

*Adanou et al
cited with Record*

tr Q9ANY1 **Pneumococcal histidine triad protein E precursor** 1039
 Q9ANY1_STRPN **(Hypothetical** AA
protein SP1004) [phtE] [Streptococcus pneumoniae] align

Score = 2016 bits (5224), Expect = 0.0
 Identities = 1004/1039 (96%), Positives = 1004/1039 (96%)

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Query: 1      MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNRRVS YVDGSQSSQKSENLTDPQVS 60
              MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNRRVS YVDGSQSSQKSENLTDPQVS
Sbjct: 1      MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNRRVS YVDGSQSSQKSENLTDPQVS 60

Query: 61     QKEGIQAEQIVIKITDQGYVTSHGDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVN 120
              QKEGIQAEQIVIKITDQGYVTSHGDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVN
Sbjct: 61     QKEGIQAEQIVIKITDQGYVTSHGDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVN 120

Query: 121    EVKGGYIIKVDGKYVYVLKDAAHADNVRTKDEINRQKQEHVKDNEKVNNSNVAVARSQGRY 180
              EVKGGYIIKVDGKYVYVLKDAAHADNVRTKDEINRQKQEHVKDNEKVNNSNVAVARSQGRY
Sbjct: 121    EVKGGYIIKVDGKYVYVLKDAAHADNVRTKDEINRQKQEHVKDNEKVNNSNVAVARSQGRY 180

Query: 181    TTNDGYVFNPADIIEDTGNAYIVPHGGHYHYIPXXXXXXXXXXXXXXXXXXXXNMQPSQLS 240
              TTNDGYVFNPADIIEDTGNAYIVPHGGHYHYIP                                NMQPSQLS
Sbjct: 181    TTNDGYVFNPADIIEDTGNAYIVPHGGHYHYIPKSDLSASELAAKAHLAKNMQPSQLS 240

Query: 241    YSSTASDNNTQSVAKGSTSKPANKSENLSLLKELYDSPSAQRYSES DGLVDFPAKIIISR 300
              YSSTASDNNTQSVAKGSTSKPANKSENLSLLKELYDSPSAQRYSES DGLVDFPAKIIISR
Sbjct: 241    YSSTASDNNTQSVAKGSTSKPANKSENLSLLKELYDSPSAQRYSES DGLVDFPAKIIISR 300

Query: 301    TPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPISGTGSTVSTNAKPNEVVXXXXXXXXXX 360
              TPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPISGTGSTVSTNAKPNEVV
Sbjct: 301    TPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPISGTGSTVSTNAKPNEVVSSLGSLSSN 360

Query: 361    XXXXXXXXKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA 420
              KELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA
Sbjct: 361    PSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA 420

Query: 421    TPSPSLPINPGTSHEKHEEDGYGFDANRIIAEDES GFVMSHGDNHYFFKKDLTEEQIKA 480
              TPSPSLPINPGTSHEKHEEDGYGFDANRIIAEDES GFVMSHGDNHYFFKKDLTEEQIKA
Sbjct: 421    TPSPSLPINPGTSHEKHEEDGYGFDANRIIAEDES GFVMSHGDNHYFFKKDLTEEQIKA 480

Query: 481    AQKHLEEVKTS HNGLDSSLSSHEQDYPSNAKEMKDLDKKIEEKIAGIMKQYGVKRESIVVN 540
              AQKHLEEVKTS HNGLDSSLSSHEQDYPSNAKEMKDLDKKIEEKIAGIMKQYGVKRESIVVN
Sbjct: 481    AQKHLEEVKTS HNGLDSSLSSHEQDYPSNAKEMKDLDKKIEEKIAGIMKQYGVKRESIVVN 540

Query: 541    KEKNAIIPYPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV 600
              KEKNAIIPYPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV
Sbjct: 541    KEKNAIIPYPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV 600

Query: 601    VNLLKNSTFNNQNF TLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVS GKVFG 660
              VNLLKNSTFNNQNF TLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVS GKVFG
Sbjct: 601    VNLLKNSTFNNQNF TLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVS GKVFG 660

Query: 661    EGVGNIANFELDQPYLPQGTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA 720
              EGVGNIANFELDQPYLPQGTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA
Sbjct: 661    EGVGNIANFELDQPYLPQGTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA 720

Query: 721    GDTYLRVNPQFAVPKGT DALVRVFDE F HGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNK 780
              GDTYLRVNPQFAVPKGT DALVRVFDE F HGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNK
Sbjct: 721    GDTYLRVNPQFAVPKGT DALVRVFDE F HGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNK 780

```

Query: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENLKLDEKVEEPKTS 840
IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENLKLDEKVEEPKTS
Sbjct: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENLKLDEKVEEPKTS 840

Query: 841 EKVEKEKLSETGNSTSNSTLEEVPTVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYL 900
EKVEKEKLSETGNSTSNSTLEEVPTVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYL
Sbjct: 841 EKVEKEKLSETGNSTSNSTLEEVPTVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYL 900

Query: 901 SGEVIKKNMADFTGEAPQGNGENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960
SGEVIKKNMADFTGEAPQGNGENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP
Sbjct: 901 SGEVIKKNMADFTGEAPQGNGENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960

Query: 961 ENSTDNGMLNPEGNGVSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTI 1020
ENSTDNGMLNPEGNGVSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTI
Sbjct: 961 ENSTDNGMLNPEGNGVSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTI 1020

Query: 1021 ELRLPSGEVIKKNLSDLIA 1039
ELRLPSGEVIKKNLSDLIA
Sbjct: 1021 ELRLPSGEVIKKNLSDLIA 1039

tr Q8DQ07 **Pneumococcal histidine triad protein E [phtE]** 1039
Q8DQ07_STRR6 **[Streptococcus** AA
pneumoniae (strain ATCC BAA-255 / R6)] align

Score = 2006 bits (5196), Expect = 0.0
Identities = 998/1039 (96%), Positives = 1000/1039 (96%)

Query: 1 MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPQVS 60
MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPQVS
Sbjct: 1 MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPQVS 60

Query: 61 QKEGIQAEQIVIKITDQGYVTSHGDIHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVN 120
QKEGIQAEQIVIKITDQGYVTSHGDIHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVN
Sbjct: 61 QKEGIQAEQIVIKITDQGYVTSHGDIHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVN 120

Query: 121 EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNNSVAVARSQGRY 180
EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNNSVAVARSQGRY
Sbjct: 121 EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNNSVAVARSQGRY 180

Query: 181 TTNDGYVFNPADIIEDTGNAYIVPHGGHYHYIPXXXXXXXXXXXXXXXXXXXXNMQPSQLS 240
TTNDGYVFNPADIIEDTGNAYIVPHGGHYHYIP NMQPSQLS
Sbjct: 181 TTNDGYVFNPADIIEDTGNAYIVPHGGHYHYIPKSDLSASELAAKAHLAKNMQPSQLS 240

Query: 241 YSSTASDNNTQSVAKGSTSKPANKSENLSLLKELYDSPAQRYSESDGLVFDPAKIISR 300
YSSTASDNNTQSVAKGSTSKPANKSENLSLLKELYDSPAQRYSESDGLVFDPAKIISR
Sbjct: 241 YSSTASDNNTQSVAKGSTSKPANKSENLSLLKELYDSPAQRYSESDGLVFDPAKIISR 300

Query: 301 TPNGVAIPHGDHYHFIPIYSKLSALEEKIARMVPISGTGSTVSTNAKPNEVVXXXXXXXXXX 360
TPNGVAIPHGDHYHFIPIYSKLSALEEKIAR VPISGTGSTVSTNAKPNEVV
Sbjct: 301 TPNGVAIPHGDHYHFIPIYSKLSALEEKIARRVPISGTGSTVSTNAKPNEVVSSLGSLSSN 360

Query: 361 XXXXXXXXKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA 420
KELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA
Sbjct: 361 PSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA 420

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Query: 421  TPSPSLPINPGTSHEKHEEDGYGFDANRIIAEDES GFVMSHGDNHNYFFKKDLTEEQIKA 480
           TPSPSLPINPG SHEKHEEDGYGFDANKRIIAEDES GF+MSHG+HNHNYFFKKDLTEEQIKA
Sbjct: 421  TPSPSLPINPGISHEKHEEDGYGFDANRIIAEDES GFIMSHGNHNYFFKKDLTEEQIKA 480

Query: 481  AQKHLEEVKTSHNGLDSLSSHEQDYPSNAKEMKDLDDKKIEEKIAGIMKQYGVKRESIVVN 540
           AQKHLEEVKTSHNGLDSLSSHEQDY P NAKEMKDLDEKTEEKIAGIMKQYGVKRESIVVN
Sbjct: 481  AQKHLEEVKTSHNGLDSLSSHEQDYPGNAKEMKDLDDKKIEEKIAGIMKQYGVKRESIVVN 540

Query: 541  KEKNAI IYPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGKNKVYTGEELTNV 600
           KEKNAI IYPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGKNKVYTGEELTNV
Sbjct: 541  KEKNAI IYPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGKNKVYTGEELTNV 600

Query: 601  VNLLKNSTFNNQNFTLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVSQKVFV 660
           VNLLKNSTFNNQNFTLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVSQKVFV
Sbjct: 601  VNLLKNSTFNNQNFTLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVSQKVFV 660

Query: 661  EGVGNIANFELDQPYLPQGTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIIFYPFHA 720
           EGVGNIANFELDQPYLPQGTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIIFYPFHA
Sbjct: 661  EGVGNIANFELDQPYLPQGTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIIFYPFHA 720

Query: 721  GDTYLRVNPQFAVPKGTDALVRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNK 780
           GDTYLRVNPQFAVPKGTDALVRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNK
Sbjct: 721  GDTYLRVNPQFAVPKGTDALVRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNK 780

Query: 781  IPVTFMANAYLDNQSTYIIVEVPILEKENQTDKPSILPQFKRNKAQENLKLDEKVEEPKTS 840
           IPVTFMANAYLDNQSTYIIVEVPILEKENQTDKPSILPQFKRNKAQEN KLDEKVEEPKTS
Sbjct: 781  IPVTFMANAYLDNQSTYIIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS 840

Query: 841  EKVEKEKLSETGNSTSNSTLEEVPVDPVQEKVAKFAESYGMKLENVLFNMDDGTIELYLP 900
           EKVEKEKLSETGNSTSNSTLEEVPVDPVQEKVAKFAESYGMKLENVLFNMDDGTIELYLP
Sbjct: 841  EKVEKEKLSETGNSTSNSTLEEVPVDPVQEKVAKFAESYGMKLENVLFNMDDGTIELYLP 900

Query: 901  SGEVIKKNMADFTGEAPQNGENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960
           SGEVIKKNMADFTGEAPQNGENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP
Sbjct: 901  SGEVIKKNMADFTGEAPQNGENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960

Query: 961  ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDDGTI 1020
           ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDDGTI
Sbjct: 961  ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDDGTI 1020

Query: 1021 ELRLPSGEVIKKNLSDLIA 1039
           ELRLPSGEVIKKNLSDLIA
Sbjct: 1021 ELRLPSGEVIKKNLSDLIA 1039

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tr Q6WNQ7 Surface protein BVH-3 [bvh-3] [Streptococcus 1039
   Q6WNQ7 STRPN pneumoniae] AA
                                align

```

Score = 2006 bits (5196), Expect = 0.0

Identities = 998/1039 (96%), Positives = 1000/1039 (96%)

```

Query: 1  MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPQVS 60
          MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPQVS
Sbjct: 1  MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPQVS 60

```

Query: 61 QKEGIQAEQIVIKITDQGYVTSHGDHYHYNGKVPYDALFSEELMKDPNYQLKDADIVN 120
QKEGIQAEQIVIKITDQGYVTSHGDHYHYNGKVPYDALFSEELMKDPNYQLKDADIVN
Sbjct: 61 QKEGIQAEQIVIKITDQGYVTSHGDHYHYNGKVPYDALFSEELMKDPNYQLKDADIVN 120

Query: 121 EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNNSNAVARSQGRY 180
EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNNSNAVARSQGRY
Sbjct: 121 EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNNSNAVARSQGRY 180

Query: 181 TTNDGYVFNPAIIEDTGNAYIVPHGGHYHYIPXXXXXXXXXXXXXXXXXXXXNMQPSQLS 240
TTNDGYVFNPAIIEDTGNAYIVPHGGHYHYIP NMQPSQLS
Sbjct: 181 TTNDGYVFNPAIIEDTGNAYIVPHGGHYHYIPKSDLSASELAAKAHLAKNMQPSQLS 240

Query: 241 YSSTASDNNTQSVAKGSTSKPANKSENLSLLKELYDSPSAQRYSESDGLVDFPAKIISR 300
YSSTASDNNTQSVAKGSTSKPANKSENLSLLKELYDSPSAQRYSESDGLVDFPAKIISR
Sbjct: 241 YSSTASDNNTQSVAKGSTSKPANKSENLSLLKELYDSPSAQRYSESDGLVDFPAKIISR 300

Query: 301 TPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPISGTGSTVSTNAKPNEVVXXXXXXXXXX 360
TPNGVAIPHGDHYHFIPYSKLSALEEKIAR VPISGTGSTVSTNAKPNEVV
Sbjct: 301 TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEVVSSLGSLSSN 360

Query: 361 XXXXXXXXKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA 420
KELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA
Sbjct: 361 PSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA 420

Query: 421 TPSPSLPINPGTSHEKHEEDGYGFDANRIIAEDES GFVMSHGDNHNYFFKKDLTEEQIKA 480
TPSPSLPINPGTSHEKHEEDGYGFDANRIIAEDES GF+MSG+HNNHYFFKKDLTEEQIKA
Sbjct: 421 TPSPSLPINPGISHEKHEEDGYGFDANRIIAEDES GFIMSHGNHNNHYFFKKDLTEEQIKA 480

Query: 481 AQKHLEEVKTSNGLDSLSSHEQDYPNAKEMKDLDDKKIEEKIAGIMKQYGVKRESIVVN 540
AQKHLEEVKTSNGLDSLSSHEQDYP NAKEMKDLDDKKIEEKIAGIMKQYGVKRESIVVN
Sbjct: 481 AQKHLEEVKTSNGLDSLSSHEQDYPGNAKEMKDLDDKKIEEKIAGIMKQYGVKRESIVVN 540

Query: 541 KEKNAIIPPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGKNKVYTGEELTNV 600
KEKNAIIPPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGKNKVYTGEELTNV
Sbjct: 541 KEKNAIIPPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGKNKVYTGEELTNV 600

Query: 601 VNLLKNSTFNNQNFLLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVSQGVFG 660
VNLLKNSTFNNQNFLLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVSQGVFG
Sbjct: 601 VNLLKNSTFNNQNFLLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVSQGVFG 660

Query: 661 EGVGNIANFELDQPYLPGQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA 720
EGVGNIANFELDQPYLPGQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA
Sbjct: 661 EGVGNIANFELDQPYLPGQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA 720

Query: 721 GDTYLRVNPQFAVPKGTDALVRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNK 780
GDTYLRVNPQFAVPKGTDALVRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNK
Sbjct: 721 GDTYLRVNPQFAVPKGTDALVRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNK 780

Query: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENLKLDEKVEEPKTS 840
IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQEN KLDEKVEEPKTS
Sbjct: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS 840

Query: 841 EKVEKEKLSETGNSTSNSTLEEVPVDPVQEKVAKFAESYGMKLENVLENMDGTIELYLP 900
EKVEKEKLSETGNSTSNSTLEEVPVDPVQEKVAKFAESYGMKLENVLENMDGTIELYLP
Sbjct: 841 EKVEKEKLSETGNSTSNSTLEEVPVDPVQEKVAKFAESYGMKLENVLENMDGTIELYLP 900

Query: 901 SGEVIKKNMADFTGEAPQGNGENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960

```

Sbjet: 901  SGEVIKKNMADFTGEAPQGNGENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960
Query: 961  ENSTDNGMLNPEGNGVSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTI 1020
           ENSTDNGMLNPEGNGVSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTI
Sbjet: 961  ENSTDNGMLNPEGNGVSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTI 1020
Query: 1021 ELRLPSGEVIKKNLSDLIA 1039
           ELRLPSGEVIKKNLSDLIA
Sbjet: 1021 ELRLPSGEVIKKNLSDLIA 1039

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tr Q6WNQ5      Surface protein BVH-3 (Fragment) [bvh-3] [Streptococcus 1019
   Q6WNQ5_STRPN pneumoniae] AA
                                align

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Score = 1974 bits (5115), Expect = 0.0
Identities = 981/1019 (96%), Positives = 981/1019 (96%)

```

Query: 21  CAYALNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPQVSQKEGIQAEQIVIKITDQGYV 80
           CAYALNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPQVSQKEGIQAEQIVIKITDQGYV
Sbjet: 1   CAYALNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPQVSQKEGIQAEQIVIKITDQGYV 60

Query: 81  TSHGDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKD 140
           TSHGDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKD
Sbjet: 61  TSHGDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKD 120

Query: 141 AAHADNVRTKDEINRQKQEHVKDNEKVNNSVAVARSQGRYTTNDGYVFNPAIIEDTGNA 200
           AAHADNVRTKDEINRQKQEHVKDNEKVNNSVAVARSQGRYTTNDGYVFNPAIIEDTGNA
Sbjet: 121 AAHADNVRTKDEINRQKQEHVKDNEKVNNSVAVARSQGRYTTNDGYVFNPAIIEDTGNA 180

Query: 201 YIVPHGGHYHYIIPXXXXXXXXXXXXXXXXXXXXNMQPSQLSYSSTASDNNTQSVAKGSTSK 260
           YIVPH GRYHYIP NMQPSQLSYSSTASDNNTQSVAKGSTSK
Sbjet: 181 YIVPHRGHYHYIPKSDLSASELAACAAHLAKNMQPSQLSYSSTASDNNTQSVAKGSTSK 240

Query: 261 PANKSENLOSLKELYDSPAQRYSSESGLVDFPAKIIISRTPNGVAIPHGDHYHFIPYSK 320
           PANKSENLOSLKELYDSPAQRYSSESGLVDFPAKIIISRTPNGVAIPHGDHYHFIPYSK
Sbjet: 241 PANKSENLOSLKELYDSPAQRYSSESGLVDFPAKIIISRTPNGVAIPHGDHYHFIPYSK 300

Query: 321 LSALEEKIARMVPISGTGSTVSTNAKPNEVVXXXXXXXXXXXXXXXXXXXXKELSSASDGYIFN 380
           LSALEEKIARMVPISGTGSTVSTNAKPNEVV KELSSASDGYIFN
Sbjet: 301 LSALEEKIARMVPISGTGSTVSTNAKPNEVVSSLGSLSSNPSSLTTSKELSSASDGYIFN 360

Query: 381 PKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLATPSPSLPINPGTSHEKHEED 440
           PKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLATPSPSLPINPGTSHEKHEED
Sbjet: 361 PKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLATPSPSLPINPGTSHEKHEED 420

Query: 441 GYGFDANRIIAEDES GFVMSHGDNHNYFFKKDLTEEQIKAAQKHLEEVKTSNGLDSLSS 500
           GYGFDANRIIAEDES GFVMSHGDNHNYFFKKDLTEEQIKAAQKHLEEVKTSNGLDSLSS
Sbjet: 421 GYGFDANRIIAEDES GFVMSHGDNHNYFFKKDLTEEQIKAAQKHLEEVKTSNGLDSLSS 480

Query: 501 HEQDYPSNAKEMKDLDDKKIEEKIAGIMKQYGVKRESIVVNKEKNAIIPHGDDHHADPID 560
           HEQDYPSNAKEMKDLDDKKIEEKIAGIMKQYGVKRESIVVNKEKNAIIPHGDDHHADPID
Sbjet: 481 HEQDYPSNAKEMKDLDDKKIEEKIAGIMKQYGVKRESIVVNKEKNAIIPHGDDHHADPID 540

Query: 561 EHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNVVNLLKNSTFNNQNFLLANGQ 620

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Sbjct: 541 EHKKPVGIGHSHSNYELFKPEEGVAKKEGKVKVYTGEEELTNVNVNLLKNSTFNNQNFTLANGQ 600

Query: 621 KRVSFSFPPELEKKLGINMLVKLITPDGKVLKVSQKVFEGGVGNIANFELDQPYLPGQT 680
KRVSFSFPPELEKKLGINMLVKLITPDGKVLKVSQKVFEGGVGNIANFELDQPYLPGQT

Sbjct: 601 KRVSFSFPPELEKKLGINMLVKLITPDGKVLKVSQKVFEGGVGNIANFELDQPYLPGQT 660

Query: 681 FKYTTIASKDYPEVSYDGTFTVPTSLAYKMASQTI FYPPFHAGDTYLRVNPQFAVPKGT DAL 740
FKYTTIASKDYPEVSYDGTFTVPTSLAYKMASQTI FYPPFHAGDTYLRVNPQFAVPKGT DAL

Sbjct: 661 FKYTTIASKDYPEVSYDGTFTVPTSLAYKMASQTI FYPPFHAGDTYLRVNPQFAVPKGT DAL 720

Query: 741 VRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVE 800
VRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVE

Sbjct: 721 VRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVE 780

Query: 801 VPILEKENQTDKPSILPQFKRNKAQENKLDEKVEE PKTSEKVEKEKLSETGNSTSNSTL 860
VPILEKENQTDKPSILPQFKRNKAQEN K DEKVEE PKTSEKVEKEKLSETGNSTSNSTL

Sbjct: 781 VPILEKENQTDKPSILPQFKRNKAQENSKFDEKVEE PKTSEKVEKEKLSETGNSTSNSTL 840

Query: 861 EEVPTVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLPSGEVIKKNMADFTGEAPQGN 920
EEVPTVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLPSGEVIKKNMADFTGEAPQGN

Sbjct: 841 EEVPTVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLPSGEVIKKNMADFTGEAPQGN 900

Query: 921 GENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKPENSTDNGMLNPEGNVGSDPM 980
GENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKPENSTDNGMLNPEGNVGSDPM

Sbjct: 901 GENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKPENSTDNGMLNPEGNVGSDPM 960

Query: 981 LDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTIELRLPSGEVIKKNLSDLIA 1039
LDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTIELRLPSGEVIKKNLSDLIA

Sbjct: 961 LDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTIELRLPSGEVIKKNLSDLIA 1019

> O < Intelligence
> O <

FASTA - Fast Pairwise Comparison of Sequences
Release 5.4

Results file SP103.res made by sdevld on Wed 28 Nov 101 11:51:05-PST.

Query sequence being compared: SP103 (1-447)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of SP103 (1-447) with:
File: US09471255-2.pep

100-
50-
M
B
E
R
O
F
S
E
U
N
C
S
SCORE 0 50 99 149 199 248 298 348 397 447
STDEV

PARAMETERS

Similarity matrix PAM-150 K-tuple 2
Threshold level of sim. 168
Gap penalty 1.00 Joining penalty 20
Gap size penalty 0.05 Window size 32
Cutoff score 0
Randomization group 0

SEARCH STATISTICS

Scores: Mean 447 Median 0 Standard Deviation 0.00
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00
Number of residues: 1039
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% similar sequence to the query sequence was found:

Init. Opt.

Sequence Name Description Length Score Score S19. Frame
1. ~~US09471255~~ sequence 2, application us/09 1039 447 447 0.00 0

1. SP103 (1-447) ~~US09471255~~ sequence 2, application ~~US09471255~~ 09/471,255

sequence 2, application us/09471255

general information:

applicant: blochem pharma inc.

applicant: hamel, jos.e

applicant: brodeur, bernard r.

applicant: pineau, isabelle

applicant: martin, denis

file of invention: novel streptococcus antigens

file reference: 12806-11pct

current application number: us/09/471,255

current filing date: 1999-12-23

prior application number: us 60/113,800

prior filing date: 1998-12-23

number of seq id nos: 102

software: fastseq for windows version 3.0

seq id no 2

length: 1039

type: prt

organism: s. pneumoniae

(linear sequence)

us-09-471-255-2 Length: 1039 November 28, 2001 11:45 Type: P Check: 8890

Initial Score = 447 Optimized Score = 447 Significance = 0.00

Residue Identity = 100% Matches = 447 Mismatches = 0

Gaps = 0 Conservative Substitutions = 0

W288/ Qwv

50 60 70 80 90 100 110 120
KITDGVYVSHQDHYHYNGKYPYALFSEELKMDPKYQLKADYINERKGYIIKVGKTYVYLKDAHA
KITDGVYVSHQDHYHYNGKYPYALFSEELKMDPKYQLKADYINERKGYIIKVGKTYVYLKDAHA
KITDGVYVSHQDHYHYNGKYPYALFSEELKMDPKYQLKADYINERKGYIIKVGKTYVYLKDAHA
130 140 150 160 170 180 190
DNVTRDEINROKOEHVKNENKYNVSNVAVARSGRRTYNDGYFNPADIEDTGNAYIVPHGSHYIKPKSD
DNVTRDEINROKOEHVKNENKYNVSNVAVARSGRRTYNDGYFNPADIEDTGNAYIVPHGSHYIKPKSD
DNVTRDEINROKOEHVKNENKYNVSNVAVARSGRRTYNDGYFNPADIEDTGNAYIVPHGSHYIKPKSD
150 160 170 180 190 200 210
LSASELAALAKAHLAGKNMOPSLSTSTASDNMTOSYAKGSTSPAKSENLOSLELYDSPSOKRYSSESD
LSASELAALAKAHLAGKNMOPSLSTSTASDNMTOSYAKGSTSPAKSENLOSLELYDSPSOKRYSSESD
LSASELAALAKAHLAGKNMOPSLSTSTASDNMTOSYAKGSTSPAKSENLOSLELYDSPSOKRYSSESD
220 230 240 250 260 270 280
GLVFDPAKIIISRPNGVVAIPHGDHFFPYKSLALEKTAIBAVPIISGTSYVSTAKANPEVSSLSGSSN
GLVFDPAKIIISRPNGVVAIPHGDHFFPYKSLALEKTAIBAVPIISGTSYVSTAKANPEVSSLSGSSN
GLVFDPAKIIISRPNGVVAIPHGDHFFPYKSLALEKTAIBAVPIISGTSYVSTAKANPEVSSLSGSSN
290 300 310 320 330 340 350 360
PSSLTTSKELSSASDGYIFNPDIYEETATAYIVRHGDHFIYIPKSNQIGOPTLPNNSLATPSPPLINPCT
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PSSLTTSKELSSASDGYIFNPDIYEETATAYIVRHGDHFIYIPKSNQIGOPTLPNNSLATPSPPLINPCT
370 380 390 400 410 420 430
410 420 430 440 450 X

Query Match 80.7%; Score 574; DB 4; Length 796;
 Best Local Similarity 80.6%; Pred. No. 4.3e-56;
 Matches 104; Conservative 16; Mismatches 9; Indels 0; Gaps 0;

Qy 8 AYALNQHRSQENKDNRRVSYVDGSQSSQSENLTPOVVSQKEGIAEQIVIKITDOGYVT 67
 Db 1 SYELGLYQARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDOGYVT 60
 Qy 68 SHGDHYHYNGKVPYDALFSEELLNKDPNYQLKDADIVNEVKGYYIIVKVDGKYYVYLKDA 127
 Db 61 SHGDHYHYNGKVPYDAIIESEELLNKDPNYKLKDEDIVNEVKGYYVIKVDGKYYVYLKDA 120
 Qy 128 AHADNVRTK 136
 Db 121 AHADNVRTK 129

SEQ ID 56 W098/18930

Query Match 80.9%; Score 575.5; DB 4; Length 763;
 Best Local Similarity 78.6%; Pred. No. 2.7e-56;
 Matches 103; Conservative 18; Mismatches 9; Indels 1; Gaps 1;

Qy 7 CAYALNQHRSQENKDNRRVSYVDGSQSSQSENLTPOVVSQKEGIAEQIVIKITDOGY 65
 Db 1 CSYELGRHOAGQVKKESNRVSYIDGQAGOKAENLTPDEVSKREGINAEQXVIKITDOGY 60
 Qy 66 VTSHGDHYHYNGKVPYDALFSEELLNKDPNYQLKDADIVNEVKGYYIIVKVDGKYYVYLK 125
 Db 61 VTSHGDHYHYNGKVPYDAIIESEELLNKDPNYQLKDSIVNEIKGGYVIKVGKYYVYLK 120
 Qy 126 DAAHADNVRTK 136
 Db 121 DAAHADNIRTK 131

W098/18930 SEQ ID 66



US006582706B1

(12) **United States Patent**
Johnson et al.

(10) **Patent No.:** US 6,582,706 B1
(45) **Date of Patent:** Jun. 24, 2003

(54) **VACCINE COMPOSITIONS COMPRISING
STREPTOCOCCUS PNEUMONIAE
POLYPEPTIDES HAVING SELECTED
STRUCTURAL MOTIFS**

(75) **Inventors:** Leslie S. Johnson, Germantown, MD
(US); John E. Adamou, Rockville, MD
(US)

(73) **Assignee:** MedImmune, Inc., Gaithersburg, MD
(US)

(*) **Notice:** Subject to any disclaimer, the term of this
patent is extended or adjusted under 35
U.S.C. 154(b) by 0 days.

(21) **Appl. No.:** 09/468,656

(22) **Filed:** Dec. 21, 1999

Related U.S. Application Data

(60) Provisional application No. 60/113,048, filed on Dec. 21,
1998.

(51) **Int. Cl.⁷** A61K 39/09

(52) **U.S. Cl.** 424/244.1; 424/184.1;
424/185.1; 424/190.1; 424/237.1; 435/69.1;
435/320.1; 530/350; 536/23.1; 536/23.7

(58) **Field of Search** 424/184.1, 185.1,
424/190.1, 237.1, 244.1; 435/69.1, 320.1;
514/94; 530/350; 536/23.1, 23.7

(56) **References Cited**

U.S. PATENT DOCUMENTS

6,042,838 A * 3/2000 Briles et al. 424/244.1

FOREIGN PATENT DOCUMENTS

WO	WO 95/06732	3/1995
WO	WO 97/48417	6/1996
WO	WO 97/41151	11/1997
WO	WO-98/18930 A2 *	5/1998
WO	WO 98/18930	5/1998
WO	WO 98/18931	5/1998
WO	WO 99/15675	4/1999
WO	WO 00/17370	3/2000
WO	WO 00/39299	7/2000

OTHER PUBLICATIONS

Paul et al. Fundamental Immunology, Raven Press, New
York, NY (1993) 3rd Edition, p. 251.*

Rifkin et al. A single amino-acid change between the
antigenically different extracellular serine proteases V2 and
B2 from *Dichelobacter nodosus*. *Gene* (1995) vol. 167, pp.
279-283.*

Abaza et al. Effects of amino acid substitutions outside an
antigenic site on protein binding to monoclonal antibodies of
predetermined specificity obtained by peptide immuniza-
tion. *Journal of Protein Chemistry* (1992) vol. 11, No. 5, pp.
433-444.*

Paul W.E. In *Fundamental Immunology* (1993) Raven Press,
New York, pp. 249-251.*

Ristori et al. Compositional bias and mimicry toward the
non-self proteome in immunodominant T cell epitopes of
self and nonself antigens. *FASEB Journal* (2000) vol. 14, pp.
431-438.*

Cundell, et al., "Receptor specificity of adherence of *Strep-
tococcus pneumoniae* to human type-11 pneumocytes and
vascular endothelial cells in vitro" *Micro. Path.* vol. 17, pp.
361-374 (1994).

Cundell et al., "*Streptococcus pneumoniae* anchor to acti-
vated human cells by the receptor for platelet-activating
factor", *Nature*, vol. 377, pp. 435-438 (1995).

Tuomanen et al., "Alcohol Consumption and Mortality
Among Women", *New Engl. J. Med.*, vol. 322, pp.
1280-1284 (1995).

Idanpaan-Heikkila et al., "Oligosaccharides Interfere with
the Establishment and Progression of Experimental Pneu-
mococcal Pneumonia", *J. Inf. Dis.*, vol. 176, pp. 704-712
(1997).

Lupas et al., "Predicting Coiled Coils from Protein
Sequences", *Sciences*, vol. 252, pp. 1162-1164 (1991).

*cited by examiner

Primary Examiner—James Housel

Assistant Examiner—Ulrike Winkler

(74) **Attorney, Agent, or Firm**—Elliot M. Olstein; Alan J.
Grant

(57) **ABSTRACT**

A vaccine composition is disclosed that comprises polypep-
tides and fragments of polypeptides containing histidine
triad residues or coiled-coil regions, some of which polypep-
tides or fragments lie between 80 and 680 residues in length.
Also disclosed are processes for preventing infection caused
by *S. pneumoniae* comprising administering of vaccine
compositions.

11 Claims, 32 Drawing Sheets

WEST Search History

Updated Search

DATE: Monday, June 20, 2005

Hide?	<u>Set</u> <u>Name</u>	<u>Query</u>	<u>Hit</u> <u>Count</u>
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<input type="checkbox"/>	L1	6582706.pn.	1
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<input type="checkbox"/>	L2	lxxc	16
<input type="checkbox"/>	L3	hxxhxxh	6
<input type="checkbox"/>	L4	htp\$2 or pht\$2 or phpa or php-a or bvh\$5 or (histidine near2 (motif or domain or triad)) or bvh3 or bvh-3 or pvh3 or pvh-3 or phtb or pht or phtd or phte or pht	14614
<input type="checkbox"/>	L5	L4 and strepto\$	1332
<input type="checkbox"/>	L6	L5 and pneumon\$	400
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<input type="checkbox"/>	L8	L7 and pneumon\$	43
<input type="checkbox"/>	L9	L7 same pneumon\$	34
		<i>DB=EPAB; PLUR=YES; OP=AND</i>	
<input type="checkbox"/>	L10	WO-200288178-A2.did.	0

END OF SEARCH HISTORY

[Generate Collection](#)[Print](#)**Search Results - Record(s) 1 through 43 of 43 returned.**

-
- ☐ 1. [20040242844](#). 16 Jul 04. 02 Dec 04. Group b streptococcus antigens and corresponding dna fragments. Martin, Denis, et al. 530/350; C07K014/00 C07K001/00 C07K017/00.
-
- ☐ 2. [20040241687](#). 18 Jun 04. 02 Dec 04. Novel compounds. Thonnard, Joelle, et al. 435/6; 424/190.1 435/252.3 435/320.1 435/69.3 530/350 536/23.7 C12Q001/68 C07H021/04 A61K039/02 C07K014/195 C12N001/21.
-
- ☐ 3. [20040203093](#). 03 Jun 02. 14 Oct 04. NUCLEOTIDE SEQUENCE OF THE HAEMOPHILUS INFLUENZAE RD GENOME, FRAGMENTS THEREOF, AND USES THEREOF. Fleischmann, Robert D., et al. 435/69.1; 435/320.1 435/325 435/6 536/23.2 702/20 C12Q001/68 G06F019/00 G01N033/48 G01N033/50 C07H021/04.
-
- ☐ 4. [20040171113](#). 19 Apr 04. 02 Sep 04. Antigens of group b streptococcus and corresponding dna fragments. Martin, Denis, et al. 435/69.1; 435/252.3 435/320.1 530/350 536/23.7 C07H021/04 C12N001/21 C07K014/315.
-
- ☐ 5. [20040110181](#). 05 Jan 04. 10 Jun 04. Novel streptococcus *pneumoniae* open reading frames encoding polypeptide antigens and uses thereof. Zagursky, Robert John, et al. 435/6; 435/252.3 435/320.1 435/69.1 530/350 536/23.7 C12Q001/68 C07H021/04 C07K014/315.
-
- ☐ 6. [20040097706](#). 18 Nov 03. 20 May 04. Streptococcus pyogenes antigens and corresponding dna fragments. Martin, Denis, et al. 530/350; 424/190.1 C07K014/315 C12Q001/68 A61K039/02.
-
- ☐ 7. [20040081662](#). 08 Oct 03. 29 Apr 04. Vaccine. Hermand, Philippe, et al. 424/190.1; A61K039/02.
-
- ☐ 8. [20040071730](#). 26 Sep 03. 15 Apr 04. Bvh-a2 and bvh-a3 antigens of group b streptococcus. Martin, Denis, et al. 424/190.1; 435/252.3 435/320.1 435/6 435/69.1 435/7.32 530/350 C07K014/315 C12N015/74 G01N033/554 G01N033/569 C12Q001/68 A61K039/02.
-
- ☐ 9. [20040052820](#). 08 Oct 02. 18 Mar 04. Fusion proteins comprising DP-178 and other viral fusion inhibitor peptides useful for treating aids. Bolognesi, Dani Paul, et al. 424/208.1; 424/188.1 424/204.1 530/300 530/350 A61K039/21 C07K014/16 A61K039/12 C07K002/00 C07K004/00 C07K005/00 C07K007/00 C07K014/00 C07K016/00 C07K017/00 A61K038/00 C07K001/00.
-
- ☐ 10. [20040052781](#). 14 Apr 03. 18 Mar 04. Vaccine compositions comprising Streptococcus *pneumoniae* polypeptides having selected structural motifs. Johnson, Leslie S., et al. 424/130.1; 424/185.1 435/100 A61K039/395 A61K039/00.
-
- ☐ 11. [20040033235](#). 06 Jan 03. 19 Feb 04. Nucleic acids encoding DP-178 and other viral fusion inhibitor peptides useful for treating aids. Bolognesi, Dani Paul, et al. 424/186.1; 424/187.1 424/188.1 424/208.1 530/350 A61K039/21 A61K039/12 C07K014/16 C07K014/10 C07K014/05 C07K014/11.
-
- ☐ 12. [20040005331](#). 13 Mar 03. 08 Jan 04. Vaccine compositions comprising Streptococcus *pneumoniae* polypeptides having selected structural motifs. Johnson, Leslie S., et al. 424/190.1; 530/350 536/23.7 A61K039/02 C07H021/04 C07K014/315.
-

-
13. [20040001836](#). 14 Apr 03. 01 Jan 04. Vaccine compositions comprising streptococcus pneumoniae polypeptides having selected structural motifs. Johnson, Leslie S., et al. 424/165.1; 424/190.1 A61K039/40 A61K039/02.
-
14. [20030204074](#). 04 Jun 03. 30 Oct 03. Streptococcus pneumoniae 37-kDa surface adhesin a protein. Sampson, Jacquelyn, et al. 536/23.7; 424/190.1 435/252.3 435/320.1 435/69.3 435/7.32 530/350 G01N033/554 G01N033/569 C07H021/04 A61K039/02 C12P021/02 C12N001/21 C07K014/315 C12N015/74.
-
15. [20030165528](#). 22 Apr 03. 04 Sep 03. Streptococcus pyogenes antigens. Martin, Denis, et al. 424/190.1; 435/252.3 435/320.1 435/69.3 530/350 536/23.7 A61K039/02 C07H021/04 C07K014/195 C12P021/02 C12N001/21 C12N015/74.
-
16. [20030105307](#). 03 Jan 01. 05 Jun 03. Streptococcus pneumoniae 37-kDa surface adhesion a protein. Sampson, Jacquelyn, et al. 536/23.1; 530/350 C07H021/02 C07H021/04 C07K001/00 C07K014/00 C07K017/00.
-
17. [20030049271](#). 21 Feb 02. 13 Mar 03. Streptococcus pyogenes polypeptides and corresponding DNA fragments. Martin, Denis, et al. 424/190.1; 435/252.3 435/320.1 435/69.3 435/7.32 530/350 536/23.7 A61K039/02 G01N033/554 G01N033/569 C07K014/315 C07H021/04 C12P021/02 C12N001/21.
-
18. [20020197605](#). 18 Dec 00. 26 Dec 02. Novel Polynucleotides. Nakagawa, Satoshi, et al. 435/6; 435/287.2 435/91.2 C12Q001/68 C12P019/34 C12M001/34.
-
19. [20020032323](#). 30 Oct 97. 14 Mar 02. STREPTOCOCCUS PNEUMONIAE POLYNUCLEOTIDES AND SEQUENCES. KUNSCH, CHARLES A., et al. 536/23.7; 435/252.3 435/320.1 435/69.1 536/24.32 C12P021/02 C07H021/04 C12N001/21 C12N015/74.
-
20. [6903184](#). 10 Jul 00; 07 Jun 05. Multiple antigenic peptides immunogenic against Streptococcus pneumoniae. Ades, Edwin W., et al. 530/300; 424/184.1 424/190.1 424/234.1 424/244.1 530/323 530/331 530/350 530/806 530/825. C07K00200 C07K00500 C07K00100 A61K03909 A61K03902.
-
21. [6833356](#). 25 Aug 00; 21 Dec 04. Pneumococcal protein homologs and fragments for vaccines. Koenig, Scott, et al. 514/12; 424/130.1 424/184.1 424/243.1 424/244.1 514/2 530/350 536/23.1. C07K014/00 A61K038/16.
-
22. [6824783](#). 07 Jun 95; 30 Nov 04. Methods for inhibition of membrane fusion-associated events, including HIV transmission. Bolognesi, Dani Paul, et al. 424/188.1; 424/208.1 435/5 530/360. A61K039/21.
-
23. [6800744](#). 30 Jun 98; 05 Oct 04. Nucleic acid and amino acid sequences relating to Streptococcus pneumoniae for diagnostics and therapeutics. Doucette-Stamm; Lynn A., et al. 536/23.1; 435/320.1 435/325 435/419 435/6 536/23.4 536/24.1 536/24.32. C12Q001/68 C12N001/14 C12N015/00 C12N005/00 C12N005/04 C07H021/02 C07H021/04.
-
24. [6783930](#). 02 Dec 99; 31 Aug 04. Development of novel anti-microbial agents based on bacteriophage genomics. Pelletier, Jerry, et al. 435/5; 435/7.1 435/7.33 435/7.8 435/883 530/350 530/820 536/23.7. C12Q001/68 G01N033/569 C07H021/04 C07K014/00.
-

- ☐ 25. 6773880. 03 Jan 01; 10 Aug 04. *Streptococcus pneumoniae* 37-kDa surface adhesion A protein. Sampson; Jacquelyn, et al. 435/6; 536/23.7 536/24.32 536/24.33. C12Q001/68.
-
- ☐ 26. 6617156. 13 Aug 98; 09 Sep 03. Nucleic acid and amino acid sequences relating to *Enterococcus faecalis* for diagnostics and therapeutics. Doucette-Stamm; Lynn A., et al. 435/320.1; 435/252.3 435/6 435/69.1 536/23.7 536/24.32. C12N015/31 C12N015/63 C12N001/13 C12Q001/68.
-
- ☐ 27. 6583275. 30 Jun 98; 24 Jun 03. Nucleic acid sequences and expression system relating to *Enterococcus faecium* for diagnostics and therapeutics. Doucette-Stamm; Lynn A., et al. 536/23.1; 435/243 435/320.1 435/325 435/6 536/24.3 536/24.32. C07H021/00 C12Q001/68 C12N015/00 C12N001/00 C12N005/00.
-
- ☐ 28. 6582706. 21 Dec 99; 24 Jun 03. Vaccine compositions comprising *Streptococcus pneumoniae* polypeptides having selected structural MOTIFS. Johnson; Leslie S., et al. 424/244.1; 424/184.1 424/185.1 424/190.1 424/237.1 435/320.1 435/69.1 530/350 536/23.1 536/23.7. A61K039/09.
-
- ☐ 29. 6562958. 04 Jun 99; 13 May 03. Nucleic acid and amino acid sequences relating to *Acinetobacter baumannii* for diagnostics and therapeutics. Breton; Gary, et al. 536/23.7; 536/23.1. C07H021/02.
-
- ☐ 30. 6551795. 18 Feb 99; 22 Apr 03. Nucleic acid and amino acid sequences relating to *pseudomonas aeruginosa* for diagnostics and therapeutics. Rubenfield; Marc J., et al. 435/69.1; 435/253.3 435/320.1 435/325 435/6 536/23.1 536/23.7. C12P021/06 C12N015/00 C07H021/04.
-
- ☐ 31. 6518013. 07 Jun 95; 11 Feb 03. Methods for the inhibition of epstein-barr virus transmission employing anti-viral peptides capable of abrogating viral fusion and transmission. Barney; Shawn O'Lin, et al. 435/5; 424/230.1 530/300 530/324 530/325 530/326. C12Q001/70.
-
- ☐ 32. 6479055. 06 Jun 95; 12 Nov 02. Methods for inhibition of membrane fusion-associated events, including respiratory syncytial virus transmission. Bolognesi; Dani Paul, et al. 424/211.1; 424/186.1 530/324. A61K039/145.
-
- ☐ 33. 6228983. 07 Jun 95; 08 May 01. Human respiratory syncytial virus peptides with antifusogenic and antiviral activities. Barney; Shawn O'Lin, et al. 530/300; 424/186.1 424/211.1 530/324 530/325 530/326. A61K038/00.
-
- ☐ 34. 6217884. 28 Dec 98; 17 Apr 01. *Streptococcus pneumoniae* 37-kDa surface adhesin a protein. Sampson; Jacquelyn S., et al. 424/244.1; 424/184.1 424/190.1 424/200.1 435/69.1 435/69.3 435/71.1 530/350 536/23.7. A61K039/09.
-
- ☐ 35. 6174860. 16 Apr 99; 16 Jan 01. Insecticidal toxins and nucleic acid sequences coding therefor. Kramer; Vance Cary, et al. 514/12; 435/320.1 435/410 435/412 435/418 435/69.1 536/23.7 800/302. A61K038/00 C12N005/02 C12N005/04 C12P021/06.
-
- ☐ 36. 5874088. 05 Jan 95; 23 Feb 99. Deletion mutants of cholera vaccines expressing heterologous antigens. Mekalanos; John J.. 424/200.1; 424/203.1 424/235.1 424/261.1 435/243 435/252.1 435/252.3 435/69.3 435/909. A61K039/106 C12N001/21.
-
- ☐ 37. 5854416. 17 Sep 96; 29 Dec 98. *Streptococcus pneumoniae* 37-KDA surface adhesin a protein and nucleic acids coding therefor. Sampson; Jacquelyn S., et al. 536/23.7; 424/244.1 435/320.1

536/23.1. C07H021/04.

☐ 38. WO 200288178A. New BVH-A4 proteins and genes from serotype III Group B streptococcus, useful for treating or preventing streptococcal infection in infants, pregnant women, non-pregnant adults (e.g. pneumonia), or members of dairy herd (mastitis). BOYER, M, et al. A61K038/00 A61K039/00 A61K039/09 A61P031/04 C07H021/04 C07K014/315 C07K019/00 C12N001/15 C12N001/19 C12N001/21 C12N005/10 C12N015/09 C12N015/31 C12N015/63 C12P021/02 G01N033/53 G01N033/569 G01N033/68.

☐ 39. WO 200231156A. New BVH-A2 and BVH-A3 antigens of Group B Streptococcus, useful for treating, preventing or diagnosing streptococcal infections, e.g. sepsis, meningitis, pneumonia, cellulitis, osteomyelitis, septic arthritis and endocarditis. BOYER, M, et al. A61K038/00 A61K039/02 A61K039/09 A61P031/04 C07K014/315 C07K019/00 C12N001/15 C12N001/19 C12N001/21 C12N005/10 C12N015/09 C12N015/31 C12N015/63 C12N015/74 C12P021/02 C12Q001/68 G01N033/554 G01N033/569.

☐ 40. WO 200222167A. Novel immunogenic composition comprising Streptococcus pneumoniae polysaccharide and protein antigen useful for preventing, ameliorating and treating pneumococcal infections in infants, toddlers and elderly persons. LAFERRIERE, C A J, et al. A61K039/09 A61K039/385 A61K039/39 A61P011/00 A61P027/16 A61P031/04.

☐ 41. WO 200222168A. New immunogenic composition for treating streptococcal infections in infants and elders, comprises two Streptococcus pneumoniae proteins selected from the poly histidine triad family and the choline binding protein family. HERMAND, P, et al. A61K000/00 A61K039/02 A61K039/09 A61K039/385 A61P011/00 A61P027/16 A61P031/04.

☐ 42. WO 200198334A. New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media, meningitis, and bacteremia. BRODEUR, B R, et al. A61K039/00 A61K039/02 A61K039/09 A61K039/39 A61P011/00 A61P027/16 A61P031/04 C07H021/04 C07K014/315 C07K019/00 C12N001/15 C12N001/19 C12N001/21 C12N005/10 C12N009/00 C12N015/09 C12N015/30 C12N015/31 C12N015/63 C12N015/74 C12P021/02 C12N015/63 C12R001:46.

☐ 43. WO 200037105A. Vaccine useful for prophylaxis and treatment of pneumococcal infections such as otitis media, nasopharyngeal and bronchial infections, comprises Streptococcus pneumoniae proteins. ADAMOU, J E, et al. A61K038/00 A61K039/00 A61K039/02 A61K039/09 A61K039/395 A61K039/40 A61P031/04 A61P031/10 C07H021/04 C07K014/315 C07K014:315.

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US006833356B1

(12) **United States Patent**
Koenig et al.

(10) **Patent No.:** US 6,833,356 B1
(45) **Date of Patent:** Dec. 21, 2004

(54) **PNEUMOCOCCAL PROTEIN HOMOLOGS
AND FRAGMENTS FOR VACCINES**

(75) **Inventors:** Scott Koenig, Rockville, MD (US); Jon
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(73) **Assignee:** Medimmune, Inc., Gaithersburg, MD
(US)

(*) **Notice:** Subject to any disclaimer, the term of this
patent is extended or adjusted under 35
U.S.C. 154(b) by 197 days.

(21) **Appl. No.:** 09/645,835

(22) **Filed:** Aug. 25, 2000

Related U.S. Application Data

(60) Provisional application No. 60/150,750, filed on Aug. 25,
1999.

(51) **Int. Cl.⁷** C07K 14/00; A61K 38/16

(52) **U.S. Cl.** 514/12; 514/2; 530/350;
424/184.1; 424/130.1; 424/243.1; 424/244.1;
536/23.1

(58) **Field of Search** 514/12, 2; 530/350,
530/23.1; 424/184.1, 130.1, 243.1, 244.1,
185.1; 536/23.1

(56) **References Cited**

U.S. PATENT DOCUMENTS

4,694,073 A * 9/1987 Bentle et al. 530/399

2003/0031682 A1 * 2/2003 Brodeur et al. 424/190.1

FOREIGN PATENT DOCUMENTS

WO	WO 98/18930	5/1998
WO	WO 99/42588	8/1999
WO	WO 00/06736	2/2000

OTHER PUBLICATIONS

Spellerberg et al., Lmb, a protein with similarities to the Lral
adhesin family, mediates attachment of streptococcus aga-
lactiae to human laminin. Infection and Immunity Feb.
1999, vol. 67 871-878.*

* cited by examiner

Primary Examiner—Robert A. Wax

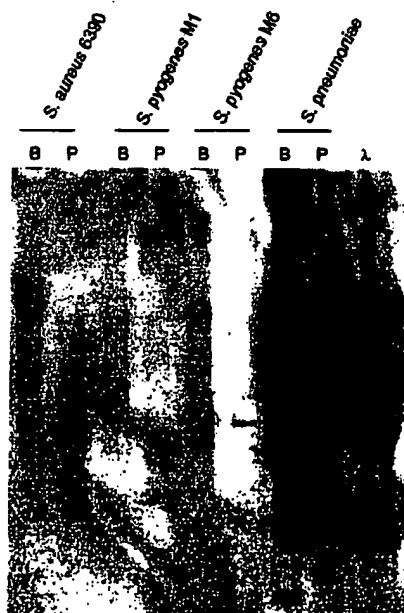
Assistant Examiner—Chih-Min Kam

(74) *Attorney, Agent, or Firm*—Elliott M. Olstein; Alan J.
Grant

(57) **ABSTRACT**

The invention is directed to isolated polypeptides bearing
sequence homology to the Sp36 protein found in pneumo-
coccal organisms, such as *Streptococcus pneumoniae*. Poly-
nucleotides encoding such polypeptides are also disclosed.
The invention also relates to antibodies specific for the
disclosed polypeptides and to uses of such antibodies in the
treatment of diseases caused by staphylococci as well as
group A and B streptococci. In addition, the invention relates
to the use of the disclosed polypeptides in compositions and
as vaccines and for prophylactic uses such as in vaccination
of animals, especially humans, against a wide variety of
streptococcal, staphylococcal and other diseases.

8 Claims, 9 Drawing Sheets



US-PAT-NO: 6833356

DOCUMENT-IDENTIFIER: US 6833356 B1

TITLE: Pneumococcal protein homologs and fragments for vaccines

DATE-ISSUED: December 21, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Koenig; Scott	Rockville	MD		
Heinrichs; Jon	North Potomac	MD		
Johnson; Leslie S.	Germantown	MD		
Adamou; John E.	Germantown	MD		

ASSIGNEE-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY	TYPE CODE
Medimmune, Inc.	Gaithersburg	MD			02

APPL-NO: 09/ 645835 [PALM]

DATE FILED: August 25, 2000

PARENT-CASE:

This application claims the priority of U.S. Provisional Application No. 60/150,750, filed Aug. 25, 1999, the disclosure of which is hereby incorporated by reference in its entirety.

INT-CL: [07] C07 K 14/00, A61 K 38/16

US-CL-ISSUED: 514/12; 514/2, 530/350, 424/184.1, 424/130.1, 424/243.1, 424/244.1, 536/23.1

US-CL-CURRENT: 514/12; 424/130.1, 424/184.1, 424/243.1, 424/244.1, 514/2, 530/350, 536/23.1

FIELD-OF-SEARCH: 514/12, 514/2, 530/350, 530/23.1, 424/184.1, 424/130.1, 424/243.1, 424/244.1, 424/185.1, 536/23.1

PRIOR-ART-DISCLOSED:

U.S. PATENT DOCUMENTS

PAT-NO	ISSUE-DATE	PATENTEE-NAME	US-CL
<input type="checkbox"/> <u>4694073</u>	September 1987	Bentle et al.	530/399
<input type="checkbox"/> <u>2003/0031682</u>	February 2003	Brodeur et al.	424/190.1

FOREIGN PATENT DOCUMENTS

FOREIGN-PAT-NO	PUBN-DATE	COUNTRY	US-CL
WO 98/18930	May 1998	WO	
WO 99/42588	August 1999	WO	
WO 00/06736	February 2000	WO	

OTHER PUBLICATIONS

Spellerberg et al., Lmb, a protein with similarities to the Lral adhesin family, mediates attachment of streptococcus agalactiae to human laminin. Infection and Immunity Feb. 1999, vol. 67 871-878.

ART-UNIT: 1653

PRIMARY-EXAMINER: Wax; Robert A.

ASSISTANT-EXAMINER: Kam; Chih-Min

ATTY-AGENT-FIRM: Olstein; Elliott M. Grant; Alan J.

ABSTRACT:

The invention is directed to isolated polypeptides bearing sequence homology to the Sp36 protein found in pneumococcal organisms, such as Streptococcus pneumoniae. Polynucleotides encoding such polypeptides are also disclosed. The invention also relates to antibodies specific for the disclosed polypeptides and to uses of such antibodies in the treatment of diseases caused by staphylococci as well as group A and B streptococci. In addition, the invention relates to the use of the disclosed polypeptides in compositions and as vaccines and for prophylactic uses such as in vaccination of animals, especially humans, against a wide variety of streptococcal, staphylococcal and other diseases.

8 Claims, 7 Drawing figures

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: Entry 15 of 34

File: USPT

Dec 21, 2004

US-PAT-NO: 6833356

DOCUMENT-IDENTIFIER: US 6833356 B1

TITLE: Pneumococcal protein homologs and fragments for vaccines

DATE-ISSUED: December 21, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Koenig; Scott	Rockville	MD		
Heinrichs; Jon	North Potomac	MD		
Johnson; Leslie S.	Germantown	MD		
Adamou; John E.	Germantown	MD		

US-CL-CURRENT: 514/12; 424/130.1, 424/184.1, 424/243.1, 424/244.1, 514/2, 530/350, 536/23.1

CLAIMS:

What is claimed is:

1. An isolated polypeptide comprising an amino acid sequence with at least 95% sequence identity to the sequence of SEQ ID NO: 4 and wherein said polypeptide binds to an antibody that is specific for Sp36 (SEQ ID NO: 7).
2. An isolated polypeptide comprising an amino acid sequence with at least 95% sequence identity to a sequence selected from the group consisting of SEQ ID NO: 2 and 4 wherein said polypeptide is identical to that found in an organism selected from the group consisting of Group A streptococci and Staphylococcus aureus and wherein said polypeptide binds to an antibody that is specific for Sp36 (SEQ ID NO: 7).
3. The isolated polypeptide of claim 2 wherein said Group A organism is Streptococcus pyogenes.
4. The isolated polypeptide of claim 2 wherein said organism is Staphylococcus aureus.
5. An isolated polypeptide comprising an amino acid sequence at least 95% identical to the sequence of SEQ ID NO: 4 and wherein said polypeptide has a sequence with at least 12.6% sequence identity to the amino acid sequence of the Sp36 protein (SEQ ID NO: 7) of Streptococcus pneumoniae and wherein said isolated polypeptide binds to an antibody that is specific for Sp36.
6. An isolated polypeptide comprising the sequence of SEQ ID NO: 2 wherein said isolated polypeptide binds to an antibody that is specific for Sp36 (SEQ ID NO: 7) of Streptococcus pneumoniae.
7. An isolated polypeptide comprising the amino acid sequence of SEQ ID NO: 2.
8. An isolated polypeptide comprising the amino acid sequence of SEQ ID NO: 4.

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L9: Entry 29 of 34

File: DWPI

Feb 10, 2005

DERWENT-ACC-NO: 2003-120461

DERWENT-WEEK: 200511

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TITLE: New BVH-A4 proteins and genes from serotype III Group B streptococcus, useful for treating or preventing streptococcal infection in infants, pregnant women, non-pregnant adults (e.g. pneumonia), or members of dairy herd (mastitis)

INVENTOR: BOYER, M; BRODEUR, B R ; HAMEL, J ; MARTIN, D ; RIOUX, S

PATENT-ASSIGNEE: SHIRE BIOCHEM INC (SHIRN), BOYER M (BOYEI), BRODEUR B R (BRODI), HAMEL J (HAMEI), MARTIN D (MARTI), RIOUX S (RIOUI)

PRIORITY-DATA: 2001US-287712P (May 2, 2001)

[Search Selected](#)[Search ALL](#)[Clear](#)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
<input type="checkbox"/> JP 2005503774 W	February 10, 2005		095	C12N015/09
<input type="checkbox"/> WO 200288178 A2	November 7, 2002	E	059	C07K014/315
<input type="checkbox"/> EP 1390505 A2	February 25, 2004	E	000	C12N015/31
<input type="checkbox"/> AU 2002308325 A1	November 11, 2002		000	C07K014/315
<input type="checkbox"/> US 20040171113 A1	September 2, 2004		000	C07H021/04

DESIGNATED-STATES: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM ZW AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR

APPLICATION-DATA:

PUB-NO	APPL-DATE	APPL-NO	DESCRIPTOR
JP2005503774W	May 2, 2002	2002JP-0585476	
JP2005503774W	May 2, 2002	2002WO-CA00664	
JP2005503774W		WO 200288178	Based on
WO 200288178A2	May 2, 2002	2002WO-CA00664	
EP 1390505A2	May 2, 2002	2002EP-0766595	
EP 1390505A2	May 2, 2002	2002WO-CA00664	
EP 1390505A2		WO 200288178	Based on
AU2002308325A1	May 2, 2002	2002AU-0308325	

AU2002308325A1		WO 200288178	Based on
US20040171113A1	May 2, 2002	2002WO-CA00664	
US20040171113A1	April 19, 2004	2004US-0476614	

INT-CL (IPC): A61 K 38/00; A61 K 39/00; A61 K 39/09; A61 P 31/04; C07 H 21/04; C07 K 14/315; C07 K 19/00; C12 N 1/15; C12 N 1/19; C12 N 1/21; C12 N 5/10; C12 N 15/09; C12 N 15/31; C12 N 15/63; C12 P 21/02; G01 N 33/53; G01 N 33/569; G01 N 33/68

ABSTRACTED-PUB-NO: WO 200288178A

BASIC-ABSTRACT:

NOVELTY - An isolated polypeptide (designated GBS-BVH-A4), which comprises a BVH-A4 protein polypeptide from serotype III Group B streptococcus (GBS) strain COH1, is new.

DETAILED DESCRIPTION - An isolated polypeptide (designated GBS-BVH-A4), which comprises a BVH-A4 protein polypeptide from serotype III Group B streptococcus (GBS) strain COH1 comprises:

- (a) a polypeptide comprising 1055 amino acids (I) fully defined in the specification;
- (b) a polypeptide having at least 80-95% identity to a second polypeptide having (I);
- (c) a polypeptide capable of raising antibodies having binding specificity for (I);
- (d) an epitope bearing portion of (a);
- (e) fragments or analogs of (a), (b), (c) or (d);
- (f) any of the polypeptides of (a)-(e), where the N-terminal Met residue is deleted; or
- (g) any of the polypeptide of (a)-(e), where the secretory amino acid sequence is deleted.

INDEPENDENT CLAIMS are also included for the following:

- (1) An isolated polynucleotide comprising a sequence:
 - (a) encoding the GBS-BVH-A4 polypeptide;
 - (b) having 3168 bp fully defined in the specification; or
 - (c) that is complementary of (a) or (b);
- (2) Vectors comprising the polynucleotide, where the DNA is operably linked to an expression control region;
- (3) Host cells comprising the vector;
- (4) Producing (M1) the GBS-BVH-A4 polypeptide;

(5) Chimeric polypeptides comprising two or more GBS-BVH-A4 polypeptides, or its fragments or analogs, provided that the polypeptides are linked so as to form a chimeric polypeptide;

(6) A pharmaceutical composition comprising the GBS-BVH-A4 polypeptide, and a pharmaceutical carrier, diluent or adjuvant;

(7) Diagnosing (M2) GBS bacterial infection in a host susceptible to GBS infection; and

(8) A kit comprising the GBS-BVH-A4 polypeptide for detecting or diagnosing streptococcal infection.

ACTIVITY - Antibiotic; Immunostimulant.

Test details are described but no results are given.

MECHANISM OF ACTION - Polypeptide Therapy; Vaccine.

Test details are described but no results are given.

USE - The GBS-BVH-A4 polypeptide is useful for the therapeutic or prophylactic treatment of GBS bacterial infection in a host susceptible to GBS infection. In particular, the GBS-BVH-A4 polypeptide is useful for treating or preventing GBS infection in a neonate or infant (e.g. sepsis, meningitis, pneumonia, cellulitis, osteomyelitis, septic arthritis, endocarditis or epiglottitis), in a pregnant woman (e.g. mild urinary tract infection to life-threatening sepsis and meningitis, osteomyelitis, endocarditis, amniotitis, endometritis, wound infection (post-cesarean or post-episiotomy), cellulitis or fasciitis), in a non-pregnant adult (e.g. bacteremia, skin or soft tissue infection, pneumonia, urosepsis, endocarditis, peritonitis, meningitis or emphysema), or in a member of dairy herd (e.g. mastitis). The composition or GBS-BVH-A4 polypeptide is also useful for treating or preventing streptococcal infection (all claimed). The GBS-BVH-A4 polypeptide or antibody is also useful for diagnosing GBS or streptococcal infection.

ABSTRACTED-PUB-NO: WO 200288178A

EQUIVALENT-ABSTRACTS:

CHOSEN-DRAWING: Dwg.0/2

DERWENT-CLASS: B04 D16

CPI-CODES: B04-B04C1; B04-C01G; B04-E01; B04-F0100E; B04-F01E; B04-N0300E; B04-N03E; B11-C07A; B11-C08E; B12-K04A4; B14-A01B2; B14-C03; B14-C09; B14-F01; B14-G01; B14-K01; B14-N01; B14-N07; B14-N16; B14-S06; B14-S11B; D05-C12; D05-H09; D05-H12A; D05-H12B; D05-H12E; D05-H14B; D05-H17A5; D05-H17B5; D05-H17C;

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DOCUMENT-IDENTIFIER: US 20040052781 A1

TITLE: Vaccine compositions comprising Streptococcus pneumoniae polypeptides having selected structural motifs

Abstract Paragraph:

A vaccine composition is disclosed that comprises polypeptides and fragments of polypeptides containing histidine triad residues or coiled-coil regions, some of which polypeptides or fragments lie between 80 and 680 residues in length. Also disclosed are processes for preventing infection caused by S. pneumoniae comprising administering of vaccine compositions.

Summary of Invention Paragraph:

[0002] This invention relates generally to the field of bacterial antigens and their use, for example, as immunogenic agents in humans and animals to stimulate an immune response. More specifically, it relates to the vaccination of mammalian species with a polypeptide comprising at least one conserved histidine triad residue (HxxHxH) and at least one helix-forming polypeptide obtained from Streptococcus pneumoniae as a mechanism for stimulating production of antibodies that protect the vaccine recipient against infection by a wide range of serotypes of pathogenic S. pneumoniae. Further, the invention relates to antibodies against such polypeptides useful in diagnosis and passive immune therapy with respect to diagnosing and treating such pneumococcal infections.

Summary of Invention Paragraph:

[0004] Streptococcus pneumoniae is a gram positive bacteria which is a major causative agent in invasive infections in animals and humans, such as sepsis, meningitis, otitis media and lobar pneumonia (Tuomanen et al. New Engl. J. Med. 322:1280-1284 (1995)). As part of the infective process, pneumococci readily bind to non-inflamed human epithelial cells of the upper and lower respiratory tract by binding to eukaryotic carbohydrates in a lectin-like manner (Cundell et al., Micro. Path. 17:361-374 (1994)). Conversion to invasive pneumococcal infections for bound bacteria may involve the local generation of inflammatory factors which may activate the epithelial cells to change the number and type of receptors on their surface (Cundell et al., Nature, 377:435-438 (1995)). Apparently, one such receptor, platelet activating factor (PAF) is engaged by the pneumococcal bacteria and within a very short period of time (minutes) from the appearance of PAF, pneumococci exhibit strongly enhanced adherence and invasion of tissue. Certain soluble receptor analogs have been shown to prevent the progression of pneumococcal infections (Idanpaan-Heikkila et al., J. Inf. Dis., 176:704-712 (1997)). A number of various other proteins have been suggested as being involved in the pathogenicity of S. pneumoniae. There remains a need for identifying polypeptides having epitopes in common from various strains of S. pneumoniae in order to utilize such polypeptides as vaccines to provide protection against a wide variety of S. pneumoniae.

Summary of Invention Paragraph:

[0005] In accordance with the present invention, there is provided vaccines and vaccine compositions that include polypeptides obtained from S. pneumoniae and/or variants of said polypeptides and/or active fragments of such polypeptides.

Brief Description of Drawings Paragraph:

[0013] FIG. 3 is a western blot demonstrating the ability of antisera raised against recombinant Sp36 derived from strain Norway type 4 to react with Sp36 of heterologous strains. Total cell lysates were immunoblotted with mouse antisera to Sp36. A band representing Sp36 protein was detected in all 23 S. pneumoniae strains tested, which included isolates from each of the 23 pneumococcal serotypes represented in the current polysaccharide vaccine.

Brief Description of Drawings Paragraph:

[0018] FIG. 8 shows the results of immunization of mice with PhtD recombinant protein, which leads to protection from lethal sepsis. C3H/HeJ (Panel A and B) or Balb/cByJ (Panel C) mice were immunized subcutaneously with PhtD protein (15 .mu.g in 50 .mu.l PBS emulsified in 50 .mu.l complete Freund's adjuvant (CFA)). The recombinant PhtD protein used in protection experiments consisted of 819 amino acid residues, starting with the cysteine (residue 20). A group of 10 sham-immunized mice received PBS with adjuvant. A second immunization of 15 .mu.g protein with incomplete Freund's adjuvant (IFA) was administered 3 weeks later; the sham group received PBS with IFA. Blood was drawn (retro-orbital bleed) at week 7; and sera from each group was pooled for analysis of anti-PhtD antibody by ELISA. Mice were challenged at week 8 by an intraperitoneal (i.p.) injection of approximately 550 CFU *S. pneumoniae* strain SJ2, serotype 6B (Panel A), 850 CFU of strain EF6796, serotype 6A (Panel B) or 450 CFU of strain EF5668, serotype 4 (Panel C). In preliminary experiments, the LD.sub.50 for strain SJ2 and EF6796 were determined to be approximately 10 CFU for both strains. The LD.sub.50 for strain EF5668 was determined to be <5 CFU. Survival was determined in all groups over the course of 15 days following challenge. Data are presented as the percent survival for a total of 10 mice per experimental group. Two-sample Log-rank test was used for statistical analysis comparing recombinant Pht immunized mice to sham-immunized mice.

Detail Description Paragraph:

[0033] In accordance with a further aspect of the invention, a vaccine of the type hereinabove described is administered for the purpose of preventing or treating infection caused by *S. pneumoniae*.

Detail Description Paragraph:

[0040] In still another aspect the present invention relates to a method of using one or more antibodies (monoclonal, polyclonal or sera) to the polypeptides of the invention as described above for the prophylaxis and/or treatment of diseases that are caused by pneumococcal bacteria. In particular, the invention relates to a method for the prophylaxis and/or treatment of infectious diseases that are caused by *S. pneumoniae*. In a still further preferred aspect, the invention relates to a method for the prophylaxis and/or treatment of otitis media, nasopharyngeal, bronchial infections, and the like in humans by utilizing a vaccine of the present invention.

Detail Description Paragraph:

[0054] The present invention further relates to variants of polynucleotides. The variants of the polynucleotides may be a naturally occurring allelic variant of the polynucleotides or a non-naturally occurring variant of the polynucleotides. The variants include variants in which one or more bases are substituted, deleted or inserted. Complements to such coding polynucleotides may be utilized to isolate polynucleotides encoding the same or similar polypeptides. In particular, such procedures are useful to obtain native immunogenic portions of polypeptides from different serotypes of *S. pneumoniae*, which is especially useful in the production of "chain" polypeptide vaccines containing multiple immunogenic segments.

Detail Description Paragraph:

[0088] The genomic DNA used as target for amplification was isolated from *S. pneumoniae* Norway strain (serotype 4), the same strain used for genomic sequencing. The complete sequence of the Sp36 gene (SEQ ID NO:9), and its predicted amino acid sequence (SEQ ID NO:8), are given in the Sequence Listing appended hereto. It was noted that the predicted amino acid sequence included a hydrophobic leader sequence followed by a sequence (LSVC) similar to the consensus sequence for Type II signal peptidase (LxxC, in which both x's typically represent small amino acids). Primers (listed as SEQ ID NOS:1-3) were designed that would amplify the Sp36 gene and allow its cloning into pQE10 and expression as a histidine-tagged protein lacking the signal sequence for purification by nickel-affinity chromatography. Cloning of the fragment amplified by SEQ ID Nos 1 and 3 would result in a protein

containing amino acids 2 through 800 of Sp36; cloning of the fragment amplified by SEQ ID Nos 2 and 3 would result in a protein containing amino acids 7 through 800 of Sp36 (amino acid numbers refer to SEQ ID NO:8).

Detail Description Paragraph:

[0090] In each of the three experiments shown in FIGS. 1A-1C, C3H/HeJ mice (10/group) were immunized intraperitoneally (i.p.) with Sp36 protein (15 .mu.g in 50 .mu.l PBS emulsified in 50 .mu.l complete Freund's adjuvant (CFA)). A group of 10 sham-immunized mice received PBS with adjuvant. A second immunization of 15 .mu.g protein with incomplete Freund's adjuvant (IFA) was administered 4 weeks later; the sham group received PBS with IFA. Blood was drawn (retro-orbital bleed) at weeks 3, 6, and 9; and sera from each group were pooled for analysis of anti-Sp36 antibody by ELISA. Mice were challenged at week 10 by an i.p. injection of approximately 500 CFU *S. pneumoniae* strain SJ2 (serotype 6B; provided by P. Flynn, St. Jude Children's Research Hospital, Memphis, Tenn.). In preliminary experiments, the LD.sub.50 of this strain was determined to be approximately 10 CFU. Mice were monitored for 14 days for survival.

Detail Description Paragraph:

[0099] C3H/HeJ mice (10 mice/group) were passively immunized by two i.p. injections of 100 .mu.l of rabbit serum. The first injection was administered twenty-four hours before challenge with 172 cfu of *S. pneumoniae* strain SJ2, and the second injection was given four hours after challenge. FIG. 2 shows the survival of mice after infection with two different strains of pneumococci.

Detail Description Paragraph:

[0102] Conservation of Sp36 Among Strains of *S. pneumoniae*

Detail Description Paragraph:

[0105] The mouse anti-Sp36 sera detected two major bands with apparent molecular weights of 97 and 100 kDa in all 23 pneumococcal lysates tested (shown in FIG. 3). The Sp36 signals obtained from *S. pneumoniae* serotypes 1, 5, 17F and 22F were lower, indicating either that the level of Sp36 expression is reduced in these strains, or that Sp36 in these strains is antigenically different.

Detail Description Paragraph:

[0112] These experiments indicate that Sp36 is recognized by the human immune system and suggest that antibodies able to bind the Sp36 protein may be produced during natural *S. pneumoniae* infection in humans. Since the patients were infected with a variety of pneumococcal strains, these data also support the idea that Sp36 is antigenically conserved.

CLAIMS:

2. A process for preventing infection caused by *S. pneumoniae* comprising: administering the vaccine of claim 1.

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L9: Entry 10 of 34

File: PGPB

Sep 4, 2003

DOCUMENT-IDENTIFIER: US 20030165528 A1

TITLE: Streptococcus pyogenes antigens

Detail Description Paragraph:

[0110] An ORF which shares 62% with the S. pyogenes BVH-Pl gene was initially presented in the patent application PCT/CA99/00114 which described Group B streptococcus antigens. BVH-PL gene was also found to share homology (62% identity) with an ORF present in the genome of S. pneumoniae (The Institute for Genomic Research).

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DOCUMENT-IDENTIFIER: US 6582706 B1

TITLE: Vaccine compositions comprising *Streptococcus pneumoniae* polypeptides having selected structural MOTIFS

Brief Summary Text (2):

This invention relates generally to the field of bacterial antigens and their use, for example, as immunogenic agents in humans and animals to stimulate an immune response. More specifically, it relates to the vaccination of mammalian species with a polypeptide comprising at least one conserved histidine triad residue (HxxHxH-SEQ ID NO: 12) and at least one helix-forming polypeptide obtained from *Streptococcus pneumoniae* as a mechanism for stimulating production of antibodies that protect the vaccine recipient against infection by a wide range of serotypes of pathogenic *S. pneumoniae*. Further, the invention relates to antibodies against such polypeptides useful in diagnosis and passive immune therapy with respect to diagnosing and treating such pneumococcal infections.

<input checked="" type="checkbox"/>	tr	Q8DQ07	_STRR6 Pneumococcal histidine triad protein E [phtE] [S...	2017	
<input checked="" type="checkbox"/>	tr	Q6WNQ7	_STRPN Surface protein BVH-3 [bvh-3] [Streptococcus pne...	2017	
<input checked="" type="checkbox"/>	tr	Q9ANY1	_STRPN Pneumococcal histidine triad protein E precursor...	2006	
<input checked="" type="checkbox"/>	tr	Q6WNQ5	_STRPN Surface protein BVH-3 (Fragment) [bvh-3] [Strept...	1968	
<input type="checkbox"/>	tr	Q8CWR4	_STRR6 Histidine Motif-Containing protein [phpA] [Strep...	442	e-
<input checked="" type="checkbox"/>	tr	Q8DPQ2	_STRR6 Pneumococcal histidine triad protein A [phtA] [S...	437	e-
<input checked="" type="checkbox"/>	tr	Q9AG74	_STRPN PhpA [phpA] [Streptococcus pneumoniae]	437	e-
<input checked="" type="checkbox"/>	tr	Q9AHT9	_STRPN Pneumococcal histidine triad A protein [phtA] [S...	435	e-
<input checked="" type="checkbox"/>	tr	Q8DQ08	_STRR6 Pneumococcal histidine triad protein D [phtD] [S...	434	e-
<input type="checkbox"/>	tr	Q6T8D7	_STRPN Pneumococcal protein BVH-11-3 [Streptococcus pne...	431	e-
<input type="checkbox"/>	tr	Q97QM8	_STRPN Conserved domain protein [SP1175] [Streptococcus...	424	e-
<input checked="" type="checkbox"/>	tr	Q9ANY2	_STRPN Pneumococcal histidine triad protein D precursor...	423	e-
<input type="checkbox"/>	tr	Q97QM9	_STRPN Conserved domain protein [SP1174] [Streptococcus...	423	e-
<input checked="" type="checkbox"/>	tr	Q9ANY3	_STRPN Pneumococcal histidine triad protein B precursor...	423	e-
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<input type="checkbox"/>	tr	Q8NZ82	_STRP8 Hypothetical protein spyM18_2072 [spyM18_2072] [...	306	1e
<input type="checkbox"/>	tr	Q8E4U1	_STRA3 Hypothetical protein gbs1306 [gbs1306] [Streptoc...	305	3e
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<input type="checkbox"/>	tr	Q9ZHG7	_STRAG Hypothetical protein [Streptococcus agalactiae]	305	4e
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<input type="checkbox"/>	tr	Q93GT5	_STRPY Histidine triad protein of group A streptococci ...	302	2e
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<input type="checkbox"/>	tr	Q9AE21	_STRAG Hypothetical protein (Fragment) [Streptococcus a...	241	9e
<input type="checkbox"/>	tr	Q8DQ06	_STRR6 Pneumococcal histidine triad protein E, truncati...	121	8e
<input type="checkbox"/>	tr	Q8E029	_STRA5 Hypothetical protein SAG0907 [SAG0907] [Streptoc...	111	1e
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<input type="checkbox"/>	tr	Q8P0G5	_STRP8 Putative internalin A [spyM18_1373] [Streptococc...	99	4e
<input type="checkbox"/>	tr	Q8K714	_STRP3 Putative internalin A [inlA] [Streptococcus pyog...	97	2e
<input type="checkbox"/>	tr	Q5XBJ5	_STRP6 Internalin protein [M6_Spy1083] [Streptococcus p...	97	3e
<input type="checkbox"/>	tr	Q99Z76	_STRPY Putative internalin A [inlA] [Streptococcus pyog...	92	9e
<input type="checkbox"/>	tr	Q5AWR8	_EMENI Hypothetical protein [AN7262.2] [Aspergillus nid...	47	0.
<input type="checkbox"/>	tr	Q6HCJ0	_BACHK Cell division protein [ftsK] [Bacillus thuringie...	47	0.
<input type="checkbox"/>	sp	P45386	IGA4_HAEIN Immunoglobulin A1 protease precursor (EC 3....	46	0.
<input type="checkbox"/>	tr	Q8ISF7	_CAEEL 2MDa_1 protein [isof] [Caenorhabditis elegans]	46	0.

<input type="checkbox"/>	tr	<u>Q8ISF6</u>	_CAEEL 2MDa_2 protein [isof] [Caenorhabditis elegans]	<u>46</u>	0.
<input type="checkbox"/>	sp	<u>P16053</u>	NFM_CHICK Neurofilament triplet M protein (160 kDa neu...	<u>45</u>	0.
<input type="checkbox"/>	sp	<u>Q97QP7</u>	IGA1A_STRPN Immunoglobulin A1 protease precursor (EC 3...	<u>44</u>	0.
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<input type="checkbox"/>	tr	<u>Q8IB63</u>	_PLAF7 Hypothetical protein PF08_0035 [PF08_0035] [Plas...	<u>44</u>	0.
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<input type="checkbox"/>	tr	<u>Q5TUJ9</u>	_ANOGA ENSANGP00000029120 [ENSANGG00000022532] [Anophel...	<u>44</u>	0.
<input type="checkbox"/>	tr	<u>Q839C3</u>	_ENTFA N-acetylmuramoyl-L-alanine amidase, family 4 [EF...	<u>44</u>	0.
<input type="checkbox"/>	tr	<u>Q7PR93</u>	_ANOGA ENSANGP00000010616 [ENSANGG00000008127] [Anophel...	<u>44</u>	0.
<input type="checkbox"/>	tr	<u>Q73793</u>	_SERCA Neurofilament medium subunit [Serinus canaria (C...	<u>43</u>	0.
<input type="checkbox"/>	tr	<u>Q9FN97</u>	_ARATH Transposon protein-like [Arabidopsis thaliana (M...	<u>43</u>	0.
<input type="checkbox"/>	tr	<u>Q54U33</u>	_DICDI Hypothetical protein [DDB0218298] [Dictyostelium...	<u>43</u>	0.
<input type="checkbox"/>	tr	<u>Q963T1</u>	_PLARE Glutamate-rich protein (Fragment) [GLURP] [Plasm...	<u>43</u>	0.
<input type="checkbox"/>	tr	<u>Q07594</u>	_ENTHI K2 protein (Fragment) [Entamoeba histolytica]	<u>43</u>	0.
<input type="checkbox"/>	tr	<u>Q6PK21</u>	_HUMAN OGFR protein [Homo sapiens (Human)]	<u>43</u>	0.
<input type="checkbox"/>	sp_vs	<u>Q9NZT2-2</u>	Splice isoform 2 of Q9NZT2 [OGFR] [Homo sapiens (...]	<u>43</u>	0.
<input type="checkbox"/>	sp	<u>Q9NZT2</u>	OGFR_HUMAN Opioid growth factor receptor (OGFr) (Zeta-...	<u>43</u>	0.
<input type="checkbox"/>	tr	<u>Q6HBX5</u>	_BACHK Hypothetical protein [BT9727_4640] [Bacillus thu...	<u>43</u>	0.
<input type="checkbox"/>	tr	<u>Q7RQS8</u>	_PLAYO Retinitis pigmentosa GTPase regulator-like prote...	<u>43</u>	0.
<input type="checkbox"/>	tr	<u>Q77320</u>	_PLAF7 Hypothetical protein MAL3P3.3 [MAL3P3.3] [Plasmo...	<u>43</u>	0.
<input type="checkbox"/>	tr	<u>Q5HQ74</u>	_STAEQ Pyruvate dehydrogenase complex E2 component, di...	<u>42</u>	0.
<input type="checkbox"/>	tr	<u>Q9L4Z1</u>	_STAEQ Pyruvate dehydrogenase complex subunit E2 [pdhC]...	<u>42</u>	0.
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<input type="checkbox"/>	tr	<u>Q90307</u>	_CARAU Carassius auratus [Carassius auratus (Goldfish)]	<u>42</u>	0.
<input type="checkbox"/>	tr	<u>Q898B0</u>	_CLOTE Hypothetical protein CTC00555 [CTC00555] [Clostr...	<u>42</u>	0.
<input type="checkbox"/>	tr	<u>Q6R4Z8</u>	_CAPBU Dehydrin cor29 [Capsella bursa-pastoris (Shepher...	<u>42</u>	0.
<input type="checkbox"/>	tr	<u>Q50R78</u>	_ENTHI Hypothetical protein [298.t00012] [Entamoeba his...	<u>42</u>	(
<input type="checkbox"/>	tr	<u>Q8MMQ1</u>	_DICDI Similar to Required for the transfer of mannosyl...	<u>42</u>	(
<input type="checkbox"/>	tr	<u>Q8IBL1</u>	_PLAF7 Hypothetical protein MAL7P1.129 [MAL7P1.129] [Pl...	<u>42</u>	(
<input type="checkbox"/>	tr	<u>Q55K21</u>	_CRYNE Hypothetical protein [CNBK1650] [Cryptococcus ne...	<u>42</u>	(
<input type="checkbox"/>	sp	<u>Q8CT13</u>	ODP2_STAEQ Dihydrolipoyllysine-residue acetyltransfera...	<u>41</u>	(
<input type="checkbox"/>	tr	<u>Q33741</u>	_STRPN SpsA protein [Streptococcus pneumoniae]	<u>41</u>	(
<input type="checkbox"/>	tr	<u>Q8I1W5</u>	_PLAF7 Hypothetical protein PFD0320c (Fragment) [PFD032...	<u>41</u>	(
<input type="checkbox"/>	tr	<u>Q5TVN3</u>	_ANOGA ENSANGP00000027660 (Fragment) [ENSANGG0000002494...	<u>41</u>	(
<input type="checkbox"/>	tr	<u>Q07593</u>	_ENTHI K2 protein (Fragment) [Entamoeba histolytica]	<u>41</u>	(
<input type="checkbox"/>	sp	<u>Q28820</u>	TRDN_RABIT Triadin [TRDN] [Oryctolagus cuniculus (Rabb...	<u>41</u>	(
<input type="checkbox"/>	sp	<u>Q59947</u>	IGA1_STRR6 Immunoglobulin A1 protease precursor (EC 3....	<u>41</u>	(
<input type="checkbox"/>	tr	<u>Q7SXW9</u>	_BRARE Wu:fc44a10 protein (Fragment) [wu:fc44a10] [Brac...	<u>41</u>	(
<input type="checkbox"/>	tr	<u>Q28688</u>	_RABIT Neurofilament-H (Fragment) [Oryctolagus cuniculu...	<u>41</u>	(
<input type="checkbox"/>	tr	<u>Q94674</u>	_PLAGA Thrombospondin-related anonymous protein (Fragme...	<u>41</u>	(
<input type="checkbox"/>	tr	<u>Q5WNG8</u>	_CAEBR Hypothetical protein CBG08011 [CBG08011] [Caenor...	<u>41</u>	(
<input type="checkbox"/>	tr	<u>Q6BLN0</u>	_DEBHA Similar to ca CA2433 IPF12959 Candida albicans I...	<u>41</u>	(
<input type="checkbox"/>	sp_vs	<u>Q28820-4</u>	Splice isoform Cardiac 3 of Q28820 [TRDN] [Orycto...	<u>41</u>	(
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<input type="checkbox"/>	sp	<u>Q54875</u>	IGA1B_STRPN Immunoglobulin A1 protease precursor (EC 3...	<u>40</u>	(

<input type="checkbox"/>	tr	<u>Q568L0</u>	_BRARE Wu:fc44a10 [wu:fc44a10] [Brachydanio rerio (Zebr....	<u>40</u>	(
<input type="checkbox"/>	tr	<u>Q4ZHU3</u>	_STAXY Biofilm-associated protein [bap] [Staphylococcus...	<u>40</u>	(
<input type="checkbox"/>	tr	<u>Q510B7</u>	_ENTHI Hypothetical protein [113.t00023] [Entamoeba his...	<u>40</u>	(
<input type="checkbox"/>	tr	<u>Q8IJ56</u>	_PLAF7 Glutamate-rich protein [PF10_0344] [Plasmodium f...	<u>40</u>	(
<input type="checkbox"/>	tr	<u>Q9GUY4</u>	_PENJP Crustocalcin [DD4(ccn)] [Penaeus japonicus (Kuru...	<u>40</u>	(
<input type="checkbox"/>	tr	<u>Q9GTX2</u>	_PLAFA Glutamate-rich protein [GLURP] [Plasmodium falci...	<u>40</u>	(
<input type="checkbox"/>	tr	<u>Q61US9</u>	_CAEBR Hypothetical protein CBG05170 [CBG05170] [Caenor...	<u>40</u>	(
<input type="checkbox"/>	tr	<u>Q6FWC0</u>	_CANGA Candida glabrata strain CBS138 chromosome D comp...	<u>40</u>	(
<input type="checkbox"/>	tr	<u>Q6CTI0</u>	_KLULA Similar to sp Q05050 Saccharomyces cerevisiae YM...	<u>40</u>	(
<input type="checkbox"/>	tr	<u>Q879S6</u>	_XYLFT Hemagglutinin-like secreted protein [pspA] [Xyle...	<u>40</u>	(
<input type="checkbox"/>	tr	<u>O17102</u>	_CAEEL Hypothetical protein F42G2.6 [F42G2.6] [Caenorha...	<u>40</u>	(

CLUSTAL W (1.74) multiple sequence alignment

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tr|Q8DQ07|Q8DQ07_STRR6      -----MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENK-DNN
tr|Q6WNQ7|Q6WNQ7_STRPN      -----MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENK-DNN
tr|Q9ANY1|Q9ANY1_STRPN      -----MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENK-DNN
tr|Q6WNQ5|Q6WNQ5_STRPN      -----CAYALNQHRSQENK-DNN
tr|Q8DPQ2|Q8DPQ2_STRR6      MQLEISNRKRVMKINKKYLVG-SAAALILSVCSYELGLYQARTVK-ENN
tr|Q9AG74|Q9AG74_STRPN      -----MKINKKYLVG-SAAALILSVCSYELGLYQARTVK-ENN
tr|Q9AHT9|Q9AHT9_STRPN      -----MKINKKYLVG-SAAALILSVCSYELGLYQARTVK-ENN
tr|Q8DQ08|Q8DQ08_STRR6      -----MKINKKYL VG-SVAVLALSVCSYELGRHQAGQVKKESN
tr|Q9ANY2|Q9ANY2_STRPN      -----MKINKKYL VG-SVAVLALSVCSYELGRHQAGQVKKESN
tr|Q9ANY3|Q9ANY3_STRPN      -----MKINKKYL VG-SVAVLALSVCSYELGRYQAGQDKKESN
                                ***  *  ::  *  ::*

tr|Q8DQ07|Q8DQ07_STRR6      RVS YVDGSQSSQKSENLT PDQVSQKEGIQAEQIVIKITDQGYVTSBGDHY
tr|Q6WNQ7|Q6WNQ7_STRPN      RVS YVDGSQSSQKSENLT PDQVSQKEGIQAEQIVIKITDQGYVTSBGDHY
tr|Q9ANY1|Q9ANY1_STRPN      RVS YVDGSQSSQKSENLT PDQVSQKEGIQAEQIVIKITDQGYVTSBGDHY
tr|Q6WNQ5|Q6WNQ5_STRPN      RVS YVDGSQSSQKSENLT PDQVSQKEGIQAEQIVIKITDQGYVTSBGDHY
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tr|Q9AG74|Q9AG74_STRPN      RVS YIDGKQATQKTENLT PDEVSKREGINAEQIVIKITDQGYVTSBGDHY
tr|Q9AHT9|Q9AHT9_STRPN      RVS YIDGKQATQKTENLT PDEVSKREGINAEQIVIKITDQGYVTSBGDHY
tr|Q8DQ08|Q8DQ08_STRR6      RVS YIDGDQAGQKAENLT PDEVSKREGINAEQIVIKITDQGYVTSBGDHY
tr|Q9ANY2|Q9ANY2_STRPN      RVS YIDGDQAGQKAENLT PDEVSKREGINAEQIVIKITDQGYVTSBGDHY
tr|Q9ANY3|Q9ANY3_STRPN      RVAYIDGDQAGQKAENLT PDEVSKREGINAEQIVIKITDQGYVTSBGDHY
                                **::**::*: **::*****::**::***:*****:*****:*****

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tr|Q6WNQ7|Q6WNQ7_STRPN      HYYNGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVY
tr|Q9ANY1|Q9ANY1_STRPN      HYYNGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVY
tr|Q6WNQ5|Q6WNQ5_STRPN      HYYNGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVY
tr|Q8DPQ2|Q8DPQ2_STRR6      HYYNGKVPYDAIFSEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVY
tr|Q9AG74|Q9AG74_STRPN      HYYNGKVPYDAI ISEELLMKDPNYQLKDEDI ISEIKGGYVIKVDGKYYVY
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tr|Q8DQ08|Q8DQ08_STRR6      HYYNGKVPYDAI ISEELLMKDPNYQLKDS DIVNEIKGGYVIKVDGKYYVY
tr|Q9ANY2|Q9ANY2_STRPN      HYYNGKVPYDAI ISEELLMKDPNYQLKDS DIVNEIKGGYVIKVDGKYYVY
tr|Q9ANY3|Q9ANY3_STRPN      HYYNGKVPYDAI ISEELLMKDPNYQLKDS DIVNEIKGGYVIKVNKYYVY
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tr|Q6WNQ7|Q6WNQ7_STRPN      LKDAAHADNVRTKDEINRQKQEHVKDNE----KVNSNVAVARSSQGRYT TN
tr|Q9ANY1|Q9ANY1_STRPN      LKDAAHADNVRTKDEINRQKQEHVKDNE----KVNSNVAVARSSQGRYT TN
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tr|Q9ANY2|Q9ANY2_STRPN      LKDAAHADNIRTKEEIKRQKQEHSHNHGG---GSNDQAVVAARAQGRYT TD
tr|Q9ANY3|Q9ANY3_STRPN      LKDAAHADNIRTKEEIKRQKQERSHNHN---SRADNAVAARAQGRYT TD
                                *****:***:***:*****: ...      :  *  **::*****:

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tr|Q6WNQ7|Q6WNQ7_STRPN      DGYVFNPADI IEDTGNAYIVPHGGHYHYIPKSDLSASELAAAKAHLAGK-
tr|Q9ANY1|Q9ANY1_STRPN      DGYVFNPADI IEDTGNAYIVPHGGHYHYIPKSDLSASELAAAKAHLAGK-
tr|Q6WNQ5|Q6WNQ5_STRPN      DGYVFNPADI IEDTGNAYIVPHRGHYHYIPKSDLSASELAAAKAHLAGK-
tr|Q8DPQ2|Q8DPQ2_STRR6      DGYIFNASDI IEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFSLGRG
tr|Q9AG74|Q9AG74_STRPN      DGYIFNASDI IEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFSLGRG
tr|Q9AHT9|Q9AHT9_STRPN      DGYIFNASDI IEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFSLGRG
tr|Q8DQ08|Q8DQ08_STRR6      DGYIFNASDI IEDTGDAYIVPHGDHYHYIPKSDLSASELAAQAAYWNGK-
tr|Q9ANY2|Q9ANY2_STRPN      DGYIFNASDI IEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAYWNGK-

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DGYIFNASDIIEDTGDAYIVPHGDHYHYI PKNELSA SELAAAEAYWNGK-
 : ** :**:***** .*****.:*****: * :

tr	Q8DQ07	Q8DQ07_	STRR6
tr	Q6WNQ7	Q6WNQ7_	STRPN
tr	Q9ANY1	Q9ANY1_	STRPN
tr	Q6WNQ5	Q6WNQ5_	STRPN
tr	Q8DPQ2	Q8DPQ2_	STRR6
tr	Q9AG74	Q9AG74_	STRPN
tr	Q9AHT9	Q9AHT9_	STRPN
tr	Q8DQ08	Q8DQ08_	STRR6
tr	Q9ANY2	Q9ANY2_	STRPN
tr	Q9ANY3	Q9ANY3_	STRPN

-----NMQP-SQLSYSSTASD---NNTQSVAKGSTSKPANKSEN
-----NMQP-SQLSYSSTASD---NNTQSVAKGSTSKPANKSEN
-----NMQP-SQLSYSSTASD---NNTQSVAKGSTSKPANKSEN
-----NMQP-SQLSYSSTASD---NNTQSVAKGSTSKPANKSEN
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-----QGSRPSSSSSYNANPAQPRLSENHNLTVTPTYHQN-QGEN
-----QGSRPSSSSSYNANPAQPRLSENHNLTVTPTYHQN-QGEN
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tr|Q8DQ07|Q8DQ07_STRR6
tr|Q6WNQ7|Q6WNQ7_STRPN
tr|Q9ANY1|Q9ANY1_STRPN
tr|Q6WNQ5|Q6WNQ5_STRPN
tr|Q8DPQ2|Q8DPQ2_STRR6
tr|Q9AG74|Q9AG74_STRPN
tr|Q9AHT9|Q9AHT9_STRPN
tr|Q8DQ08|Q8DQ08_STRR6
tr|Q9ANY2|Q9ANY2_STRPN
tr|Q9ANY3|Q9ANY3_STRPN
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LQSLKELYDSPSAQRYSESDGLVFDPAKIIISRTPNGVAIPHGDHYHFIP
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LQSLKELYDSPSAQRYSESDGLVFDPAKIIISRTPNGVAIPHGDHYHFIP
LQSLKELYDSPSAQRYSESDGLVFDPAKIIISRTPNGVAIPHGDHYHFIP
IDSLKQLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIP
IDSLKQLYKLPLSQRHVESDGLIFDPAQITSRTANGVAVPHGDHYHFIP
IDSLKQLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIP
ISSLLRELYAKPLSERHVESDGLIFDPAQITSRTANGVAVPHGDHYHFIP
ISSLLRELYAKPLSERHVESDGLIFDPAQITSRTARGVAVPHGNHYHFIP
ISSLLRELYAKPLSERHVESDGLIFDPAQITSRTARGVAVPHGNHYHFIP
* . * * . * * * * . * . * * * * * * * * * * * * * * * * * * *

```
tr|Q8DQ07|Q8DQ07_STRR6
tr|Q6WNQ7|Q6WNQ7_STRPN
tr|Q9ANY1|Q9ANY1_STRPN
tr|Q6WNQ5|Q6WNQ5_STRPN
tr|Q8DPQ2|Q8DPQ2_STRR6
tr|Q9AG74|Q9AG74_STRPN
tr|Q9AHT9|Q9AHT9_STRPN
tr|Q8DQ08|Q8DQ08_STRR6
tr|Q9ANY2|Q9ANY2_STRPN
tr|Q9ANY3|Q9ANY3_STRPN
```

YSKLSALEEIKIARRVPISGTGSTVSTNAKPNEVVSSLGSLSSNPS---SL
YSKLSALEEIKIARRVPISGTGSTVSTNAKPNEVVSSLGSLSSNPS---SL
YSKLSALEEIKIARMVPISGTGSTVSTNAKPNEVVSSLGSLSSNPS---SL
YSKLSALEEIKIARMVPISGTGSTVSTNAKPNEVVSSLGSLSSNPS---SL
YSQMSELEERIARI I PLRYRSNHWVPDSRP-EQPS PQTPPEPS PG-----
YSQLSPLEEKLARI I PLRYRSNHWVPDSRP-EQPS PQTPPEPS PSPQPAP
YSQMSELEERIARI I PLRYRSNHWVPDSRP-EQPS PQTPPEPS PG-----
YSQLSPLEEKLARI I PLRYRSNHWVPDSRP-EQPS PQTPPEPS PSPQPAP
YEQMSELEKRIARI I PLRYRSNHWVPDSRP-EQPS PQTPPEPS PSPQPAP
YEQMSELEKRIARI I PLRYRSNHWVPDSRP-EQPS PQTPPEPS PS-----
* . . . * * * *

```
tr|Q8DQ07|Q8DQ07_STRR6
tr|Q6WNQ7|Q6WNQ7_STRPN
tr|Q9ANY1|Q9ANY1_STRPN
tr|Q6WNQ5|Q6WNQ5_STRPN
tr|Q8DPQ2|Q8DPQ2_STRR6
tr|Q9AG74|Q9AG74_STRPN
tr|Q9AHT9|Q9AHT9_STRPN
tr|Q8DQ08|Q8DQ08_STRR6
tr|Q9ANY2|Q9ANY2_STRPN
tr|Q9ANY3|Q9ANY3_STRPN
```

TTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTL
TTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTL
TTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTL
TTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTL
-PQPAPNLKIDSNSSLVSQLVRKVGEgyVFEEKGISRYVFAKD-----L
NPQPAPSNPIDEK--LVKEAVRKVGdgyVFEENGVPryIPAKD-----L
-PQPAPNLKIDSNSSLVSQLVRKVGEgyVFEEKGISRYVFAKD-----L
NPQPAPSNPIDEK--LVKEAVRKVGdgyVFEENGVPryIPAKD-----L
NPQPAPSNPIDEK--LVKEAVRKVGdgyVFEENGVSryIPAKD-----L
-PQPAPSNPIDGK--LVKEAVRKVGdgyVFEENGVSryIPAKD-----L

 * * * * *
 * * * * *

```
tr|Q8DQ07|Q8DQ07_STRR6
tr|Q6WNQ7|Q6WNQ7_STRPN
tr|Q9ANY1|Q9ANY1_STRPN
tr|Q6WNQ5|Q6WNQ5_STRPN
tr|Q8DPQ2|Q8DPQ2_STRR6
tr|Q9AG74|Q9AG74_STRPN
tr|Q9AHT9|Q9AHT9_STRPN
tr|Q8DQ08|Q8DQ08_STRR6
tr|Q9ANY2|Q9ANY2_STRPN
```

PNNSLATPSPSLPINPGISHEKHEEDGYGFDANRIIAEDES GFIMSHGNH
PNNSLATPSPSLPINPGISHEKHEEDGYGFDANRIIAEDES GFIMSHGNH
PNNSLATPSPSLPINPGTSHEKHEEDGYGFDANRIIAEDES GFVMSHGDH
PNNSLATPSPSLPINPGTSHEKHEEDGYGFDANRIIAEDES GFVMSHGDH
PSETVKNLESKLSKQESVSHT-----LTAKKEN---VAPRDQ
SAETAAGIDSKLAKQESLSHK-----LGAKKTD---LPSSDR
PSETVKNLESKLSKQESVSHT-----LTAKKEN---VAPRDQ
SAETAAGIDSKLAKQESLSHK-----LGAKKTD---LPSSDR
SAETAAGIDSKLAKQESLSHK-----LGAKKTD---LPSSDR

tr Q9ANY3 Q9ANY3_STRPN	SAETAAGIDSKLAKQESLSHK-----LGTKKTD---LPSSDR .: . . . * . : . ** : : . . : . :
tr Q8DQ07 Q8DQ07_STRR6	NHYFFKKDLTEEQIKAAQKHLEEVKTSHNGLDSLSSHEQDYPGNAKEMKD
tr Q6WNQ7 Q6WNQ7_STRPN	NHYFFKKDLTEEQIKAAQKHLEEVKTSHNGLDSLSSHEQDYPGNAKEMKD
tr Q9ANY1 Q9ANY1_STRPN	NHYFFKKDLTEEQIKAAQKHLEEVKTSHNGLDSLSSHEQDYPGNAKEMKD
tr Q6WNQ5 Q6WNQ5_STRPN	NHYFFKKDLTEEQIKAAQKHLEEVKTSHNGLDSLSSHEQDYPGNAKEMKD
tr Q8DPQ2 Q8DPQ2_STRR6	EFYDKAYNLLTEAHKALFEN-KGRNSDFQALDKLLERLNDEST-----N
tr Q9AG74 Q9AG74_STRPN	EFYNKAYDLLARIHQDLLDN-KGRQVDFEALDNLLERLKDVS-----D
tr Q9AHT9 Q9AHT9_STRPN	EFYDKAYNLLTEAHKALFXN-KGRNSDFQALDKLLERLNDEST-----N
tr Q8DQ08 Q8DQ08_STRR6	EFYNKAYDLLARIHQDLLDN-KGRQVDFEALDNLLERLKDVS-----D
tr Q9ANY2 Q9ANY2_STRPN	EFYNKAYDLLARIHQDLLDN-KGRQVDFEALDNLLERLKDVP-----D
tr Q9ANY3 Q9ANY3_STRPN	EFYNKAYDLLARIHQDLLDN-KGRQVDFEALDNLLERLKDVS-----D :. * : * . : : : : . . . * . * . : : * . :
tr Q8DQ07 Q8DQ07_STRR6	LDKKIEEKIAGIMKQYGVKRESIVVNKEKNAIYPHGDHHDADPIDEHKP
tr Q6WNQ7 Q6WNQ7_STRPN	LDKKIEEKIAGIMKQYGVKRESIVVNKEKNAIYPHGDHHDADPIDEHKP
tr Q9ANY1 Q9ANY1_STRPN	LDKKIEEKIAGIMKQYGVKRESIVVNKEKNAIYPHGDHHDADPIDEHKP
tr Q6WNQ5 Q6WNQ5_STRPN	LDKKIEEKIAGIMKQYGVKRESIVVNKEKNAIYPHGDHHDADPIDEHKP
tr Q8DPQ2 Q8DPQ2_STRR6	KEKLVDLLAFLAPITHPER----LGKPN SQIEYTE-----DEVRIAQL
tr Q9AG74 Q9AG74_STRPN	KVKLVDDILAFLAPIRHPER----LGKPN AQITYTD-----DEIQVAKL
tr Q9AHT9 Q9AHT9_STRPN	KEKLVDLLAFLAPITHPER----LGKPN SQIEYTE-----DEVRIAQL
tr Q8DQ08 Q8DQ08_STRR6	KVKLVDDILAFLAPIRHPER----LGKPN AQITYTD-----DEIQVAKL
tr Q9ANY2 Q9ANY2_STRPN	KVKLVDDILAFLAPIRHPER----LGKPN AQITYTD-----DEIQVAKL
tr Q9ANY3 Q9ANY3_STRPN	KVKLVDDILAFLAPIRHPER----LGKPN AQITYTD-----DEIQVAKL * : : : * : : * : : * : : * : : *
tr Q8DQ07 Q8DQ07_STRR6	VGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNVNNLLKNSTFNNQNF
tr Q6WNQ7 Q6WNQ7_STRPN	VGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNVNNLLKNSTFNNQNF
tr Q9ANY1 Q9ANY1_STRPN	VGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNVNNLLKNSTFNNQNF
tr Q6WNQ5 Q6WNQ5_STRPN	VGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNVNNLLKNSTFNNQNF
tr Q8DPQ2 Q8DPQ2_STRR6	ADK-YTTSDGYIFDEHD-IISDEGD-AYVTPHMGHS-HWIKKDSLSEAER
tr Q9AG74 Q9AG74_STRPN	AGK-YTTEDGYIFDPRD-ITSDEGD-AYVTPHMGHS-HWIKKDSLSEAER
tr Q9AHT9 Q9AHT9_STRPN	ADK-YTTSDGYIFDEHD-IISDEGD-AYVTPHMGHS-HWIKKDSLSEAER
tr Q8DQ08 Q8DQ08_STRR6	AGK-YTTEDGYIFDPRD-ITSDEGD-AYVTPHMGHS-HWIKKDSLSEAER
tr Q9ANY2 Q9ANY2_STRPN	AGK-YTTEDGYIFDPRD-ITSDEGD-AYVTPHMGHS-HWIKKDSLSEAER
tr Q9ANY3 Q9ANY3_STRPN	AGK-YTAEDGYIFDPRD-ITSDEGD-AYVTPHMGHS-HWIKKDSLSEAER .. : : : * . : : . . * . : * . : : : : : :
tr Q8DQ07 Q8DQ07_STRR6	TLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVSQKVFGEVGV
tr Q6WNQ7 Q6WNQ7_STRPN	TLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVSQKVFGEVGV
tr Q9ANY1 Q9ANY1_STRPN	TLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVSQKVFGEVGV
tr Q6WNQ5 Q6WNQ5_STRPN	TLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVSQKVFGEVGV
tr Q8DPQ2 Q8DPQ2_STRR6	VAAQAYTKEKGILPPSPDADVKN-----PTGDSAAAIYNRVKGE---
tr Q9AG74 Q9AG74_STRPN	AAAQAYAKEKGLTPPSTDHQDSGN-----TEAKGAEAIYNRVKAA---
tr Q9AHT9 Q9AHT9_STRPN	VAAQAYTKEKGILPPSPDADVKN-----PTGDSAAAIYNRVKGE---
tr Q8DQ08 Q8DQ08_STRR6	AAAQAYAKEKGLTPPSTDHQDSGN-----TEAKGAEAIYNRVKAA---
tr Q9ANY2 Q9ANY2_STRPN	AAAQAYAKEKGLTPPSTDHQDSGN-----TEAKGAEAIYNRVKAA---
tr Q9ANY3 Q9ANY3_STRPN	AAAQAYAXEKGLTPPSTDHQDSGN-----TEAKGAEAIYNRVKAA--- . * . . . * . : . * . . . : : * .
tr Q8DQ07 Q8DQ07_STRR6	NIANFELDQPYLPQGTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTI
tr Q6WNQ7 Q6WNQ7_STRPN	NIANFELDQPYLPQGTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTI
tr Q9ANY1 Q9ANY1_STRPN	NIANFELDQPYLPQGTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTI
tr Q6WNQ5 Q6WNQ5_STRPN	NIANFELDQPYLPQGTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTI
tr Q8DPQ2 Q8DPQ2_STRR6	--KRIPLVR--LP-YMVEHTVEVK-----NGNLIIP--HKDHYHNIK
tr Q9AG74 Q9AG74_STRPN	--KKVPLDR--MP-YNLQYTVEVK-----NGSLIIP--HYDHYHNIK
tr Q9AHT9 Q9AHT9_STRPN	--KRIPLVR--LP-YMVEHTVEVK-----NGNLIIP--HKDHYHNIK
tr Q8DQ08 Q8DQ08_STRR6	--KKVPLDR--MP-YNLQYTVEVK-----NGSLIIP--HYDHYHNIK
tr Q9ANY2 Q9ANY2_STRPN	--KKVPLDR--MP-YNLQYTVEVK-----NGSLIIP--HYDHYHNIK


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tr|Q9ANY3|Q9ANY3_STRPN      --KKVPLDR--MP-YNLQYTVEVK-----NGSLIIP---HYDHYHNIK
.. * : : * : : * : * : : * : : :

tr|Q8DQ07|Q8DQ07_STRR6      FYPFHAGDTYLRVNPQFAVPKGTDALVRVFDEFHGNAYLENNYKVGEIKL
tr|Q6WNQ7|Q6WNQ7_STRPN      FYPFHAGDTYLRVNPQFAVPKGTDALVRVFDEFHGNAYLENNYKVGEIKL
tr|Q9ANY1|Q9ANY1_STRPN      FYPFHAGDTYLRVNPQFAVPKGTDALVRVFDEFHGNAYLENNYKVGEIKL
tr|Q6WNQ5|Q6WNQ5_STRPN      FYPFHAGDTYLRVNPQFAVPKGTDALVRVFDEFHGNAYLENNYKVGEIKL
tr|Q8DPQ2|Q8DPQ2_STRR6      FAWFDDH-----TYKAPNG-YTLEDLFATIK--YYVEHPDER-----
tr|Q9AG74|Q9AG74_STRPN      FEWFDEG-----LYEAPKG-YSLEDLLATVK--YYVEHPNER-----
tr|Q9AHT9|Q9AHT9_STRPN      FAWFDDH-----TYKAPNG-YTLEDLFATIK--YYVEHPDER-----
tr|Q8DQ08|Q8DQ08_STRR6      FEWFDEG-----LYEAPKG-YSLEDLLATVK--YYVEHPNER-----
tr|Q9ANY2|Q9ANY2_STRPN      FEWFDEG-----LYEAPKG-YSLEDLLATVK--YYVEHPNER-----
tr|Q9ANY3|Q9ANY3_STRPN      FEWFDEG-----LYEAPKG-YSLEDLLATVK--YYVEHPNER-----
* * : : * : * : : * : : :

tr|Q8DQ07|Q8DQ07_STRR6      PIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVEVP----ILEKENQT
tr|Q6WNQ7|Q6WNQ7_STRPN      PIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVEVP----ILEKENQT
tr|Q9ANY1|Q9ANY1_STRPN      PIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVEVP----ILEKENQT
tr|Q6WNQ5|Q6WNQ5_STRPN      PIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVEVP----ILEKENQT
tr|Q8DPQ2|Q8DPQ2_STRR6      --PHSNDG----WGN-----ASEHVLGKK-----DHS
tr|Q9AG74|Q9AG74_STRPN      --PHSDNG----FGN-----ASDHVQRNKGQ-----ADTNQT
tr|Q9AHT9|Q9AHT9_STRPN      --PHSNDG----WGN-----ASEHVLGKK-----DHS
tr|Q8DQ08|Q8DQ08_STRR6      --PHSDNG----FGN-----ASDHVQRNKGQADTNQTEKPNEEKPQT
tr|Q9ANY2|Q9ANY2_STRPN      --PHSDNG----FGN-----ASDHVRKNK-----VDQD
tr|Q9ANY3|Q9ANY3_STRPN      --PHSDNG----FGN-----ASDHVQRNKGQ-----ADTNQT
* : : * * * : : : :

tr|Q8DQ07|Q8DQ07_STRR6      DKPSILPQFKRKAQENSKLDEKVEEPKTSEKVEKEKLSETGNSTSNSTL
tr|Q6WNQ7|Q6WNQ7_STRPN      DKPSILPQFKRKAQENSKLDEKVEEPKTSEKVEKEKLSETGNSTSNSTL
tr|Q9ANY1|Q9ANY1_STRPN      DKPSILPQFKRKAQENSKLDEKVEEPKTSEKVEKEKLSETGNSTSNSTL
tr|Q6WNQ5|Q6WNQ5_STRPN      DKPSILPQFKRKAQENSKLDEKVEEPKTSEKVEKEKLSETGNSTSNSTL
tr|Q8DPQ2|Q8DPQ2_STRR6      EDP-----NKNFKADEEPVE--ETP-AEP-----
tr|Q9AG74|Q9AG74_STRPN      EKP-----NEEKPOTEKPEE--ETPREEK-PSEKPEP-----
tr|Q9AHT9|Q9AHT9_STRPN      EDP-----NKNFKADEEPVE--ETP-AEP-----
tr|Q8DQ08|Q8DQ08_STRR6      EKP-----EEDKEHDEVSEP--THPESDEK-ENHVGLNPS-ADN
tr|Q9ANY2|Q9ANY2_STRPN      SKP-----DEDKEHDEVSEP--THPESDEK-ENHAGLNPS-ADN
tr|Q9ANY3|Q9ANY3_STRPN      EKP-----SEEKPOTEKPEE--ETPREEK-PSEKPEP-----
.. * : : * : : :

tr|Q8DQ07|Q8DQ07_STRR6      EEVPTVDPVQEKVAKFAESYG-MKLENVLFNMDGTIELYLPSGEVIKKNM
tr|Q6WNQ7|Q6WNQ7_STRPN      EEVPTVDPVQEKVAKFAESYG-MKLENVLFNMDGTIELYLPSGEVIKKNM
tr|Q9ANY1|Q9ANY1_STRPN      EEVPTVDPVQEKVAKFAESYG-MKLENVLFNMDGTIELYLPSGEVIKKNM
tr|Q6WNQ5|Q6WNQ5_STRPN      EEVPTVDPVQEKVAKFAESYG-MKLENVLFNMDGTIELYLPSGEVIKKNM
tr|Q8DPQ2|Q8DPQ2_STRR6      -----E-----VPQVET---EKVEAQLKEAEVLLAKV
tr|Q9AG74|Q9AG74_STRPN      --KPTEEPEEESPEESPE---ESEEPQVET---EKVKEKLREAEADLLGKI
tr|Q9AHT9|Q9AHT9_STRPN      -----E-----VPQVET---EKVEAQLKEAEVLLAKV
tr|Q8DQ08|Q8DQ08_STRR6      LYKPSTDTEE-TEEEAEDTTDEAEIPQVEH---SVINAKIAEAEALLEKV
tr|Q9ANY2|Q9ANY2_STRPN      LYKPSTDTEE-TEEEAEDTTDEAEIPQVEN---SVINAKIADAEALLEKV
tr|Q9ANY3|Q9ANY3_STRPN      --KPTEEPEE-SPEESEE-----PQVET---EKVEEKLREAEADLLGKI
: : * : : : :

tr|Q8DQ07|Q8DQ07_STRR6      ADFTGEAPQNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVK
tr|Q6WNQ7|Q6WNQ7_STRPN      ADFTGEAPQNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVK
tr|Q9ANY1|Q9ANY1_STRPN      ADFTGEAPQNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVK
tr|Q6WNQ5|Q6WNQ5_STRPN      ADFTGEAPQNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVK
tr|Q8DPQ2|Q8DPQ2_STRR6      TDSS--LKANATETLAGLRNNLTQIMDNN-SIMAEAEKLLALLKGS--N
tr|Q9AG74|Q9AG74_STRPN      QNPI--IKSNAKETLTGLKNNLLFGTQDNN-TIMAEAEKLLALLKGS--K
tr|Q9AHT9|Q9AHT9_STRPN      TDSS--LKANATETLAGLRNNLTQIMDNN-SIMAEAEKLLALLKGS--N
tr|Q8DQ08|Q8DQ08_STRR6      TDSS--IRQNAVETLTGLKSSLLLGTKDNN-TISAEVDSLLALLKES--Q
tr|Q9ANY2|Q9ANY2_STRPN      TDPS--IRQNAVETLTGLKSSLLLGTKDNN-TISAEVDSLLALLKES--Q

```

tr Q9ANY3 Q9ANY3_STRPN	QDPI--IKSNAKETLTGLKNNLLFGTQDNN-TIMAEAEKLLALLKES--K : . * : * : . . *
tr Q8DQ07 Q8DQ07_STRR6	PENSTDNGMLNPEGNGVSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGL
tr Q6WNQ7 Q6WNQ7_STRPN	PENSTDNGMLNPEGNGVSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGL
tr Q9ANY1 Q9ANY1_STRPN	PENSTDNGMLNPEGNGVSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGL
tr Q6WNQ5 Q6WNQ5_STRPN	PENSTDNGMLNPEGNGVSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGL
tr Q8DPQ2 Q8DPQ2_STRR6	PSSVSKEKIN-----
tr Q9AG74 Q9AG74_STRPN	-----
tr Q9AHT9 Q9AHT9_STRPN	PSSVSKEKIN-----
tr Q8DQ08 Q8DQ08_STRR6	PTPIQ-----
tr Q9ANY2 Q9ANY2_STRPN	PAPIQ-----
tr Q9ANY3 Q9ANY3_STRPN	-----
tr Q8DQ07 Q8DQ07_STRR6	DSVIFNMDGTIELRLPSGEVIKKNLSDLIA
tr Q6WNQ7 Q6WNQ7_STRPN	DSVIFNMDGTIELRLPSGEVIKKNLSDLIA
tr Q9ANY1 Q9ANY1_STRPN	DSVIFNMDGTIELRLPSGEVIKKNLSDLIA
tr Q6WNQ5 Q6WNQ5_STRPN	DSVIFNMDGTIELRLPSGEVIKKNLSDLIA
tr Q8DPQ2 Q8DPQ2_STRR6	-----
tr Q9AG74 Q9AG74_STRPN	-----
tr Q9AHT9 Q9AHT9_STRPN	-----
tr Q8DQ08 Q8DQ08_STRR6	-----
tr Q9ANY2 Q9ANY2_STRPN	-----
tr Q9ANY3 Q9ANY3_STRPN	-----

FileUp

MSF: 1080 Type: P Check: 8540 ..

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Name: tr|Q8DQ07|Q8DQ07_STRR6 oo Len: 1080 Check: 6992 Weight: 0.100
Name: tr|Q6WNQ7|Q6WNQ7_STRPN oo Len: 1080 Check: 6992 Weight: 0.100
Name: tr|Q9ANY1|Q9ANY1_STRPN oo Len: 1080 Check: 7347 Weight: 0.100
Name: tr|Q6WNQ5|Q6WNQ5_STRPN oo Len: 1080 Check: 4063 Weight: 0.100
Name: tr|Q8DPQ2|Q8DPQ2_STRR6 oo Len: 1080 Check: 1836 Weight: 0.100
Name: tr|Q9AG74|Q9AG74_STRPN oo Len: 1080 Check: 8409 Weight: 0.100
Name: tr|Q9AHT9|Q9AHT9_STRPN oo Len: 1080 Check: 9461 Weight: 0.100
Name: tr|Q8DQ08|Q8DQ08_STRR6 oo Len: 1080 Check: 9939 Weight: 0.100
Name: tr|Q9ANY2|Q9ANY2_STRPN oo Len: 1080 Check: 1016 Weight: 0.100
Name: tr|Q9ANY3|Q9ANY3_STRPN oo Len: 1080 Check: 2485 Weight: 0.100

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tr|Q8DQ07|Q8DQ07_STRR6 ..... ..MKFSKKYI AAGSAVIVSL SLCAYALNQH RSQENK.DNN
tr|Q6WNQ7|Q6WNQ7_STRPN ..... ..MKFSKKYI AAGSAVIVSL SLCAYALNQH RSQENK.DNN
tr|Q9ANY1|Q9ANY1_STRPN ..... ..MKFSKKYI AAGSAVIVSL SLCAYALNQH RSQENK.DNN
tr|Q6WNQ5|Q6WNQ5_STRPN ..... ..CAYALNQH RSQENK.DNN
tr|Q8DPQ2|Q8DPQ2_STRR6 MQLEISNRKR VSMKINKKYL VG.SAAALIL SVCSYELGLY QARTVK.ENN
tr|Q9AG74|Q9AG74_STRPN ..... ..MKINKKYL VG.SAAALIL SVCSYELGLY QARTVK.ENN
tr|Q9AHT9|Q9AHT9_STRPN ..... ..MKINKKYL VG.SAAALIL SVCSYELGLY QARTVK.ENN
tr|Q8DQ08|Q8DQ08_STRR6 ..... ..MKINKKYL AG.SVAVLAL SVCSYELGRH QAGQVKKESN
tr|Q9ANY2|Q9ANY2_STRPN ..... ..MKINKKYL AG.SVAVLAL SVCSYELGRH QAGQVKKESN
tr|Q9ANY3|Q9ANY3_STRPN ..... ..MKINKKYL AG.SVAVLAL SVCSYELGRY QAGQDKKESN

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tr|Q8DQ07|Q8DQ07_STRR6 RVSYVDGSQS SQKSENLTDP QVSQKEGIQA EQIVIKITDQ GYVTSHGDHY
tr|Q6WNQ7|Q6WNQ7_STRPN RVSYVDGSQS SQKSENLTDP QVSQKEGIQA EQIVIKITDQ GYVTSHGDHY
tr|Q9ANY1|Q9ANY1_STRPN RVSYVDGSQS SQKSENLTDP QVSQKEGIQA EQIVIKITDQ GYVTSHGDHY
tr|Q6WNQ5|Q6WNQ5_STRPN RVSYVDGSQS SQKSENLTDP QVSQKEGIQA EQIVIKITDQ GYVTSHGDHY
tr|Q8DPQ2|Q8DPQ2_STRR6 RVSYIDGKQA TQKTENLTDP EVSKREGINA EQIVIKITDQ GYVTSHGDHY
tr|Q9AG74|Q9AG74_STRPN RVSYIDGKQA TQKTENLTDP EVSKREGINA EQIVIKITDQ GYVTSHGDHY
tr|Q9AHT9|Q9AHT9_STRPN RVSYIDGKQA TQKTENLTDP EVSKREGINA EQIVIKITDQ GYVTSHGDHY
tr|Q8DQ08|Q8DQ08_STRR6 RVSYIDGDQA GQKAENLTDP EVSKREGINA EQIVIKITDQ GYVTSHGDHY
tr|Q9ANY2|Q9ANY2_STRPN RVSYIDGDQA GQKAENLTDP EVSKREGINA EQIVIKITDQ GYVTSHGDHY
tr|Q9ANY3|Q9ANY3_STRPN RVAYIDGDQA GQKAENLTDP EVSKREGINA EQIVIKITDQ GYVTSHGDHY

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```

tr|Q8DQ07|Q8DQ07_STRR6 HYYNGKVPYD ALFSEELLMK DPNYQLKDAD IVNEVKGGYI IKVDGKYYVY
tr|Q6WNQ7|Q6WNQ7_STRPN HYYNGKVPYD ALFSEELLMK DPNYQLKDAD IVNEVKGGYI IKVDGKYYVY
tr|Q9ANY1|Q9ANY1_STRPN HYYNGKVPYD ALFSEELLMK DPNYQLKDAD IVNEVKGGYI IKVDGKYYVY
tr|Q6WNQ5|Q6WNQ5_STRPN HYYNGKVPYD ALFSEELLMK DPNYQLKDAD IVNEVKGGYI IKVDGKYYVY
tr|Q8DPQ2|Q8DPQ2_STRR6 HYYNGKVPYD AIFSEELLMK DPNYKLKDED IVNEVKGGYV IKVDGKYYVY
tr|Q9AG74|Q9AG74_STRPN HYYNGKVPYD AIISEELLMK DPNYQLKDED IISEIKGGYV IKVDGKYYVY
tr|Q9AHT9|Q9AHT9_STRPN HYYNGKVPYD AIISEELLMK DPNYKLKDED IVNEVKGGYV IKVDGKYYVY
tr|Q8DQ08|Q8DQ08_STRR6 HYYNGKVPYD AIISEELLMK DPNYQLKDSD IVNEIKGGYV IKVDGKYYVY
tr|Q9ANY2|Q9ANY2_STRPN HYYNGKVPYD AIISEELLMK DPNYQLKDSD IVNEIKGGYV IKVDGKYYVY
tr|Q9ANY3|Q9ANY3_STRPN HYYNGKVPYD AIISEELLMK DPNYQLKDSD IVNEIKGGYV IKVNGKYYVY

```

```

tr|Q8DQ07|Q8DQ07_STRR6 LKDAAHADNV RTKDEINRQK QEHVKDNE.. ..KVNSNVAV ARSQGRYTTN
tr|Q6WNQ7|Q6WNQ7_STRPN LKDAAHADNV RTKDEINRQK QEHVKDNE.. ..KVNSNVAV ARSQGRYTTN
tr|Q9ANY1|Q9ANY1_STRPN LKDAAHADNV RTKDEINRQK QEHVKDNE.. ..KVNSNVAV ARSQGRYTTN

```

tr Q6WNQ5 Q6WNQ5_STRPN	LKDAAHADNV	RTKDEINRQK	QEHVKDNE..	..KVNSNVAV	ARSQGRYTTN
tr Q8DPQ2 Q8DPQ2_STRR6	LKDAAHADNV	RTKEEINRQK	QEHSQHREGG	TPRNDGAVAL	ARSQGRYTTD
tr Q9AG74 Q9AG74_STRPN	LKDAAHADNV	RTKEEINRQK	QEHSQHREGG	TPRNDGAVAL	ARSQGRYTTD
tr Q9AHT9 Q9AHT9_STRPN	LKDAAHADNV	RTKEEINRQK	QEHSQHREGG	TPRNDGAVAL	ARSQGRYTTD
tr Q8DQ08 Q8DQ08_STRR6	LKDAAHADNI	RTKEEIKRQK	QERSHNNH..	.SRADNAVAA	ARAQGRYTTD
tr Q9ANY2 Q9ANY2_STRPN	LKDAAHADNI	RTKEEIKRQK	QESHSHNHGG.	.GSNDQAVVA	ARAQGRYTTD
tr Q9ANY3 Q9ANY3_STRPN	LKDAAHADNI	RTKEEIKRQK	QERSHNNH..	.SRADNAVAA	ARAQGRYTTD

tr Q8DQ07 Q8DQ07_STRR6	DGYVFNPADI	IEDTGNAYIV	PHGGHYHYIP	KSDLSASELA	AAKAHLAGK.
tr Q6WNQ7 Q6WNQ7_STRPN	DGYVFNPADI	IEDTGNAYIV	PHGGHYHYIP	KSDLSASELA	AAKAHLAGK.
tr Q9ANY1 Q9ANY1_STRPN	DGYVFNPADI	IEDTGNAYIV	PHGGHYHYIP	KSDLSASELA	AAKAHLAGK.
tr Q6WNQ5 Q6WNQ5_STRPN	DGYVFNPADI	IEDTGNAYIV	PHRGHYHYIP	KSDLSASELA	AAKAHLAGK.
tr Q8DPQ2 Q8DPQ2_STRR6	DGYIFNASDI	IEDTGDAYIV	PHGDHYHYIP	KNELSASELA	AAEAFLSGRG
tr Q9AG74 Q9AG74_STRPN	DGYIFNASDI	IEDTGDAYIV	PHGDHYHYIP	KNELSASELA	AAEAFLSGRG
tr Q9AHT9 Q9AHT9_STRPN	DGYIFNASDI	IEDTGDAYIV	PHGDHYHYIP	KNELSASELA	AAEAFLSGRG
tr Q8DQ08 Q8DQ08_STRR6	DGYIFNASDI	IEDTGDAYIV	PHGDHYHYIP	KSDLSASELA	AAQAYWNGK.
tr Q9ANY2 Q9ANY2_STRPN	DGYIFNASDI	IEDTGDAYIV	PHGDHYHYIP	KNELSASELA	AAEAYWNGK.
tr Q9ANY3 Q9ANY3_STRPN	DGYIFNASDI	IEDTGDAYIV	PHGDHYHYIP	KNELSASELA	AAEAYWNGK.

tr Q8DQ07 Q8DQ07_STRR6NMQP:SQLS	YSSTASD...	NNTQSVAKGS	TSKPANKSEN
tr Q6WNQ7 Q6WNQ7_STRPNNMQP:SQLS	YSSTASD...	NNTQSVAKGS	TSKPANKSEN
tr Q9ANY1 Q9ANY1_STRPNNMQP:SQLS	YSSTASD...	NNTQSVAKGS	TSKPANKSEN
tr Q6WNQ5 Q6WNQ5_STRPNNMQP:SQLS	YSSTASD...	NNTQSVAKGS	TSKPANKSEN
tr Q8DPQ2 Q8DPQ2_STRR6	NLSNSRITYRR	QNSDNTSRTN	WVPSVSNPGT	TNTNTSNNSN	TNSQASQSDN
tr Q9AG74 Q9AG74_STRPN	NLSNSRITYRR	QNSDNTSRTN	WVPSVSNPGT	TNTNTSNNSN	TNSQASQSDN
tr Q9AHT9 Q9AHT9_STRPN	NLSNSRITYRR	QNSDNTSRTN	WVPSVSNPGT	TNTNTSNNSN	TNSQASQSDN
tr Q8DQ08 Q8DQ08_STRR6	QGSRPSSSSS	HNANPAQPR	SENHNLTVTP	TYHQN.QGEN
tr Q9ANY2 Q9ANY2_STRPN	QGSRPSSSSS	YNANPAQPR	SENHNLTVTP	TYHQN.QGEN
tr Q9ANY3 Q9ANY3_STRPN	QGSRPSSSSS	YNANPAQPR	SENHNLTVTP	TYHQN.QGEN

tr Q8DQ07 Q8DQ07_STRR6	LQSLKELYD	SPSAQRYSES	DGLVFDPAKI	ISRTPNGVAI	PHGDHYHFIP
tr Q6WNQ7 Q6WNQ7_STRPN	LQSLKELYD	SPSAQRYSES	DGLVFDPAKI	ISRTPNGVAI	PHGDHYHFIP
tr Q9ANY1 Q9ANY1_STRPN	LQSLKELYD	SPSAQRYSES	DGLVFDPAKI	ISRTPNGVAI	PHGDHYHFIP
tr Q6WNQ5 Q6WNQ5_STRPN	LQSLKELYD	SPSAQRYSES	DGLVFDPAKI	ISRTPNGVAI	PHGDHYHFIP
tr Q8DPQ2 Q8DPQ2_STRR6	IDSLLKQLYK	LPLSQRHVES	DGLVFDPAQI	TSRTARGVAV	PHGDHYHFIP
tr Q9AG74 Q9AG74_STRPN	IDSLLKQLYK	LPLSQRHVES	DGLIFDPAQI	TSRTANGVAV	PHGDHYHFIP
tr Q9AHT9 Q9AHT9_STRPN	IDSLLKQLYK	LPLSQRHVES	DGLVFDPAQI	TSRTARGVAV	PHGDHYHFIP
tr Q8DQ08 Q8DQ08_STRR6	ISSLLRELYA	KPLSERHVES	DGLIFDPAQI	TSRTANGVAV	PHGDHYHFIP
tr Q9ANY2 Q9ANY2_STRPN	ISSLLRELYA	KPLSERHVES	DGLIFDPAQI	TSRTARGVAV	PHGNHYHFIP
tr Q9ANY3 Q9ANY3_STRPN	ISSLLRELYA	KPLSERHVES	DGLIFDPAQI	TSRTARGVAV	PHGNHYHFIP

tr Q8DQ07 Q8DQ07_STRR6	YSKLSALEEK	IARRVPISGT	GSTVSTNAKP	NEVVSSLGSL	SSNPS...SL
tr Q6WNQ7 Q6WNQ7_STRPN	YSKLSALEEK	IARRVPISGT	GSTVSTNAKP	NEVVSSLGSL	SSNPS...SL
tr Q9ANY1 Q9ANY1_STRPN	YSKLSALEEK	IARMVPISGT	GSTVSTNAKP	NEVVSSLGSL	SSNPS...SL
tr Q6WNQ5 Q6WNQ5_STRPN	YSKLSALEEK	IARMVPISGT	GSTVSTNAKP	NEVVSSLGSL	SSNPS...SL
tr Q8DPQ2 Q8DPQ2_STRR6	YSQMSELEER	IARIIPLYR	SNHWVPDSRP	.EQPSPQPTP	EPSPG.....
tr Q9AG74 Q9AG74_STRPN	YSQLSPLEEK	LARIIPLYR	SNHWVPDSRP	.EQPSPQSTP	EPSPSPQPAP
tr Q9AHT9 Q9AHT9_STRPN	YSQMSELEER	IARIIPLYR	SNHWVPDSRP	.EQPSPQPTP	EPSPG.....
tr Q8DQ08 Q8DQ08_STRR6	YSQLSPLEEK	LARIIPLYR	SNHWVPDSRP	.EQPSPQSTP	EPSPSPQPAP
tr Q9ANY2 Q9ANY2_STRPN	YEQMSELEKR	IARIIPLYR	SNHWVPDSRP	.EQPSPQSTP	EPSPSPQPAP
tr Q9ANY3 Q9ANY3_STRPN	YEQMSELEKR	IARIIPLYR	SNHWVPDSRP	.EESPQPTP	EPSPS.....

tr Q8DQ07 Q8DQ07_STRR6	TTSKELSSAS	DGYIFNPKDI	VEETATAYIV	RHGDHFHYIP	KSNQIGQPTL
tr Q6WNQ7 Q6WNQ7_STRPN	TTSKELSSAS	DGYIFNPKDI	VEETATAYIV	RHGDHFHYIP	KSNQIGQPTL
tr Q9ANY1 Q9ANY1_STRPN	TTSKELSSAS	DGYIFNPKDI	VEETATAYIV	RHGDHFHYIP	KSNQIGQPTL

tr Q6WNQ5 Q6WNQ5_STRPN	TTSKELSSAS	DGYIFNPKDI	VEETATAYIV	RHGDHFHYIP	KSNQIGQPTL
tr Q8DPQ2 Q8DPQ2_STRR6	.PQPAPNLKI	DSNSSLVSQL	VRKVGEGYVF	EEKGISRYVF	AKD.....L
tr Q9AG74 Q9AG74_STRPN	NPQPAPSNPI	DEK..LVKEA	VRKVGEGYVF	EENGVPYRIP	AKD.....L
tr Q9AHT9 Q9AHT9_STRPN	.PQPAPNLKI	DSNSSLVSQL	VRKVGEGYVF	EEKGISRYVF	AKD.....L
tr Q8DQ08 Q8DQ08_STRR6	NPQPAPSNPI	DEK..LVKEA	VRKVGEGYVF	EENGVPYRIP	AKD.....L
tr Q9ANY2 Q9ANY2_STRPN	NPQPAPSNPI	DEK..LVKEA	VRKVGEGYVF	EENGVSRYIP	AKD.....L
tr Q9ANY3 Q9ANY3_STRPN	.PQPAPSNPI	DGK..LVKEA	VRKVGEGYVF	EENGVSRYIP	AKD.....L

tr Q8DQ07 Q8DQ07_STRR6	PNNSLATPSP	SLPINPGISH	EKHEEDGYGF	DANRIIAEDE	SGFIMSHGNH
tr Q6WNQ7 Q6WNQ7_STRPN	PNNSLATPSP	SLPINPGISH	EKHEEDGYGF	DANRIIAEDE	SGFIMSHGNH
tr Q9ANY1 Q9ANY1_STRPN	PNNSLATPSP	SLPINPGTSH	EKHEEDGYGF	DANRIIAEDE	SGFVMSHGDH
tr Q6WNQ5 Q6WNQ5_STRPN	PNNSLATPSP	SLPINPGTSH	EKHEEDGYGF	DANRIIAEDE	SGFVMSHGDH
tr Q8DPQ2 Q8DPQ2_STRR6	PSETVKNLES	KLSKQESVSH	T.....LTAKKE	N...VAPRDQ
tr Q9AG74 Q9AG74_STRPN	SAETAAGIDS	KLAKQESLSH	K.....LGAKKT	D...LPSSDR
tr Q9AHT9 Q9AHT9_STRPN	PSETVKNLES	KLSKQESVSH	T.....LTAKKE	N...VAPRDQ
tr Q8DQ08 Q8DQ08_STRR6	SAETAAGIDS	KLAKQESLSH	K.....LGAKKT	D...LPSSDR
tr Q9ANY2 Q9ANY2_STRPN	SAETAAGIDS	KLAKQESLSH	K.....LGAKKT	D...LPSSDR
tr Q9ANY3 Q9ANY3_STRPN	SAETAAGIDS	KLAKQESLSH	K.....LGTKKT	D...LPSSDR

tr Q8DQ07 Q8DQ07_STRR6	NHYFFKKDLT	EEQIKAAQKH	LEEVTSHNG	LDSLSSHEQD	YPGNAKEMKD
tr Q6WNQ7 Q6WNQ7_STRPN	NHYFFKKDLT	EEQIKAAQKH	LEEVTSHNG	LDSLSSHEQD	YPGNAKEMKD
tr Q9ANY1 Q9ANY1_STRPN	NHYFFKKDLT	EEQIKAAQKH	LEEVTSHNG	LDSLSSHEQD	YPSNAKEMKD
tr Q6WNQ5 Q6WNQ5_STRPN	NHYFFKKDLT	EEQIKAAQKH	LEEVTSHNG	LDSLSSHEQD	YPSNAKEMKD
tr Q8DPQ2 Q8DPQ2_STRR6	EFYDKAYNLL	TEAHKALFEN	.KGRNSDFQA	LDKLLERLND	EST.....N
tr Q9AG74 Q9AG74_STRPN	EFYNKAYDLL	ARIHQDLLDN	.KGRQVDFEA	LDNLLERLKD	VSS.....D
tr Q9AHT9 Q9AHT9_STRPN	EFYDKAYNLL	TEAHKALFXN	.KGRNSDFQA	LDKLLERLND	EST.....N
tr Q8DQ08 Q8DQ08_STRR6	EFYNKAYDLL	ARIHQDLLDN	.KGRQVDFEA	LDNLLERLKD	VSS.....D
tr Q9ANY2 Q9ANY2_STRPN	EFYNKAYDLL	ARIHQDLLDN	.KGRQVDFEA	LDNLLERLKD	VPS.....D
tr Q9ANY3 Q9ANY3_STRPN	EFYNKAYDLL	ARIHQDLLDN	.KGRQVDFEA	LDNLLERLKD	VSS.....D

tr Q8DQ07 Q8DQ07_STRR6	LDKKIEEKIA	GIMKQYGVKR	ESIVVNKEKN	AIIPPHGDHH	HADPIDEHKP
tr Q6WNQ7 Q6WNQ7_STRPN	LDKKIEEKIA	GIMKQYGVKR	ESIVVNKEKN	AIIPPHGDHH	HADPIDEHKP
tr Q9ANY1 Q9ANY1_STRPN	LDKKIEEKIA	GIMKQYGVKR	ESIVVNKEKN	AIIPPHGDHH	HADPIDEHKP
tr Q6WNQ5 Q6WNQ5_STRPN	LDKKIEEKIA	GIMKQYGVKR	ESIVVNKEKN	AIIPPHGDHH	HADPIDEHKP
tr Q8DPQ2 Q8DPQ2_STRR6	KEKLVDLLA	FLAPITHPERLGKPNS	QIEYTE....	..DEVRIAQL
tr Q9AG74 Q9AG74_STRPN	KVKLVDDILA	FLAPIRHPERLGKPNA	QITYTD....	..DEIQVAKL
tr Q9AHT9 Q9AHT9_STRPN	KEKLVDLLA	FLAPITHPERLGKPNS	QIEYTE....	..DEVRIAQL
tr Q8DQ08 Q8DQ08_STRR6	KVKLVDDILA	FLAPIRHPERLGKPNA	QITYTD....	..DEIQVAKL
tr Q9ANY2 Q9ANY2_STRPN	KVKLVDDILA	FLAPIRHPERLGKPNA	QITYTD....	..DEIQVAKL
tr Q9ANY3 Q9ANY3_STRPN	KVKLVDDILA	FLAPIRHPERLGKPNA	QITYTD....	..DEIQVAKL

tr Q8DQ07 Q8DQ07_STRR6	VGIGHSHSNY	ELFKPEEGVA	KKEGNKVYTG	EELTNVNNLL	KNSTFNNQNF
tr Q6WNQ7 Q6WNQ7_STRPN	VGIGHSHSNY	ELFKPEEGVA	KKEGNKVYTG	EELTNVNNLL	KNSTFNNQNF
tr Q9ANY1 Q9ANY1_STRPN	VGIGHSHSNY	ELFKPEEGVA	KKEGNKVYTG	EELTNVNNLL	KNSTFNNQNF
tr Q6WNQ5 Q6WNQ5_STRPN	VGIGHSHSNY	ELFKPEEGVA	KKEGNKVYTG	EELTNVNNLL	KNSTFNNQNF
tr Q8DPQ2 Q8DPQ2_STRR6	ADK.YTTSDG	YIFDEHD.II	SDEGD.AYVT	PHMGHS.HWI	GKDSLSDKEK
tr Q9AG74 Q9AG74_STRPN	AGK.YTTEDG	YIFDPRD.IT	SDEGD.AYVT	PHMTHS.HWI	KKDSLSEAER
tr Q9AHT9 Q9AHT9_STRPN	ADK.YTTSDG	YIFDEHD.II	SDEGD.AYVT	PHMGHS.HWI	GKDSLSDKEK
tr Q8DQ08 Q8DQ08_STRR6	AGK.YTTEDG	YIFDPRD.IT	SDEGD.AYVT	PHMTHS.HWI	KKDSLSEAER
tr Q9ANY2 Q9ANY2_STRPN	AGK.YTTEDG	YIFDPRD.IT	SDEGD.AYVT	PHMTHS.HWI	KKDSLSEAER
tr Q9ANY3 Q9ANY3_STRPN	AGK.YTAEDG	YIFDPRD.IT	SDEGD.AYVT	PHMTHS.HWI	KKDSLSEAER

tr Q8DQ07 Q8DQ07_STRR6	TLANGQKRVS	FSFPPELEKK	LGINMLVKLI	TPDGKVLEKV	SGKVFEGGVG
tr Q6WNQ7 Q6WNQ7_STRPN	TLANGQKRVS	FSFPPELEKK	LGINMLVKLI	TPDGKVLEKV	SGKVFEGGVG
tr Q9ANY1 Q9ANY1_STRPN	TLANGQKRVS	FSFPPELEKK	LGINMLVKLI	TPDGKVLEKV	SGKVFEGGVG

tr Q6WNQ5 Q6WNQ5_STRPN	TLANGQKRVS	FSFPPELEKK	LGINMLVKLI	TPDGKVLEKV	SGKVFGEVGVG
tr Q8DPQ2 Q8DPQ2_STRR6	VAAQAYTKEK	GILPPSPDAD	VKAN.....	.PTGDSAAAI	YNRVKGE...
tr Q9AG74 Q9AG74_STRPN	AAAQAYAKEK	GLTPPSTDHQ	DSGN.....	.TEAKGAEAI	YNRVKAA...
tr Q9AHT9 Q9AHT9_STRPN	VAAQAYTKEK	GILPPSPDAD	VKAN.....	.PTGDSAAAI	YNRVKGE...
tr Q8DQ08 Q8DQ08_STRR6	AAAQAYAKEK	GLTPPSTDHQ	DSGN.....	.TEAKGAEAI	YNRVKAA...
tr Q9ANY2 Q9ANY2_STRPN	AAAQAYAKEK	GLTPPSTDHQ	DSGN.....	.TEAKGAEAI	YNRVKAA...
tr Q9ANY3 Q9ANY3_STRPN	AAAQAYAXEK	GLTPPSTDHQ	DSGN.....	.TEAKGAEAI	YNRVKAA...

tr Q8DQ07 Q8DQ07_STRR6	NIANFELDQP	YLPQGTFKYT	IASKDYPEVS	YDGTFTVPTS	LAYKMASQTI
tr Q6WNQ7 Q6WNQ7_STRPN	NIANFELDQP	YLPQGTFKYT	IASKDYPEVS	YDGTFTVPTS	LAYKMASQTI
tr Q9ANY1 Q9ANY1_STRPN	NIANFELDQP	YLPQGTFKYT	IASKDYPEVS	YDGTFTVPTS	LAYKMASQTI
tr Q6WNQ5 Q6WNQ5_STRPN	NIANFELDQP	YLPQGTFKYT	IASKDYPEVS	YDGTFTVPTS	LAYKMASQTI
tr Q8DPQ2 Q8DPQ2_STRR6	..KRIPLVR.	.LP.YMVEHT	VEVK.....	.NGNLIIP..	.HKDHYHNIK
tr Q9AG74 Q9AG74_STRPN	..KKVPLDR.	.MP.YNLQYT	VEVK.....	.NGSLIIP..	.HYDHYHNIK
tr Q9AHT9 Q9AHT9_STRPN	..KRIPLVR.	.LP.YMVEHT	VEVK.....	.NGNLIIP..	.HKDHYHNIK
tr Q8DQ08 Q8DQ08_STRR6	..KKVPLDR.	.MP.YNLQYT	VEVK.....	.NGSLIIP..	.HYDHYHNIK
tr Q9ANY2 Q9ANY2_STRPN	..KKVPLDR.	.MP.YNLQYT	VEVK.....	.NGSLIIP..	.HYDHYHNIK
tr Q9ANY3 Q9ANY3_STRPN	..KKVPLDR.	.MP.YNLQYT	VEVK.....	.NGSLIIP..	.HYDHYHNIK

tr Q8DQ07 Q8DQ07_STRR6	FYPFHAGDTY	LRVNPQFAVP	KGTDALVRVF	DEFHGNAYLE	NNYKVGEIKL
tr Q6WNQ7 Q6WNQ7_STRPN	FYPFHAGDTY	LRVNPQFAVP	KGTDALVRVF	DEFHGNAYLE	NNYKVGEIKL
tr Q9ANY1 Q9ANY1_STRPN	FYPFHAGDTY	LRVNPQFAVP	KGTDALVRVF	DEFHGNAYLE	NNYKVGEIKL
tr Q6WNQ5 Q6WNQ5_STRPN	FYPFHAGDTY	LRVNPQFAVP	KGTDALVRVF	DEFHGNAYLE	NNYKVGEIKL
tr Q8DPQ2 Q8DPQ2_STRR6	FAWFDDH...TYKAP	NG.YTLEDLF	ATIK..YYVE	HPDER.....
tr Q9AG74 Q9AG74_STRPN	FEWFDEG...LYEAP	KG.YSLEDLL	ATVK..YYVE	HPNER.....
tr Q9AHT9 Q9AHT9_STRPN	FAWFDDH...TYKAP	NG.YTLEDLF	ATIK..YYVE	HPDER.....
tr Q8DQ08 Q8DQ08_STRR6	FEWFDEG...LYEAP	KG.YSLEDLL	ATVK..YYVE	HPNER.....
tr Q9ANY2 Q9ANY2_STRPN	FEWFDEG...LYEAP	KG.YTLEDLL	ATVK..YYVE	HPNER.....
tr Q9ANY3 Q9ANY3_STRPN	FEWFDEG...LYEAP	KG.YTLEDLL	ATVK..YYVE	HPNER.....

tr Q8DQ07 Q8DQ07_STRR6	PIPKLNQGT	RTAGNKIPVT	FMANAYLDNQ	STYIVEVP..	..ILEKENQT
tr Q6WNQ7 Q6WNQ7_STRPN	PIPKLNQGT	RTAGNKIPVT	FMANAYLDNQ	STYIVEVP..	..ILEKENQT
tr Q9ANY1 Q9ANY1_STRPN	PIPKLNQGT	RTAGNKIPVT	FMANAYLDNQ	STYIVEVP..	..ILEKENQT
tr Q6WNQ5 Q6WNQ5_STRPN	PIPKLNQGT	RTAGNKIPVT	FMANAYLDNQ	STYIVEVP..	..ILEKENQT
tr Q8DPQ2 Q8DPQ2_STRR6	..PHSNDG..	..WGN.....	..ASEHVLGK	K.....DHS
tr Q9AG74 Q9AG74_STRPN	..PHSNDG..	..FGN.....	..ASDHVQRN	KNGQ.....ADTNQT
tr Q9AHT9 Q9AHT9_STRPN	..PHSNDG..	..WGN.....	..ASEHVLGK	K.....DHS
tr Q8DQ08 Q8DQ08_STRR6	..PHSDNG..	..FGN.....	..ASDHVQRN	KNGQADTNQT	EKPNEEKPQT
tr Q9ANY2 Q9ANY2_STRPN	..PHSDNG..	..FGN.....	..ASDHVRKN	K.....VDQD
tr Q9ANY3 Q9ANY3_STRPN	..PHSDNG..	..FGN.....	..ASDHVQRN	KNGQ.....ADTNQT

tr Q8DQ07 Q8DQ07_STRR6	DKPSILPQFK	RNKAQENSKL	DEKVEEPKTS	EKVEKEKLSE	TGNSTSNSTL
tr Q6WNQ7 Q6WNQ7_STRPN	DKPSILPQFK	RNKAQENSKL	DEKVEEPKTS	EKVEKEKLSE	TGNSTSNSTL
tr Q9ANY1 Q9ANY1_STRPN	DKPSILPQFK	RNKAQENLKL	DEKVEEPKTS	EKVEKEKLSE	TGNSTSNSTL
tr Q6WNQ5 Q6WNQ5_STRPN	DKPSILPQFK	RNKAQENSKF	DEKVEEPKTS	EKVEKEKLSE	TGNSTSNSTL
tr Q8DPQ2 Q8DPQ2_STRR6	EDP.....NKNFKA	DEEPVE..ET	P.AEP.....
tr Q9AG74 Q9AG74_STRPN	EKP.....NEEKPO	TEKPEE..ET	PREEKP.QSE	KPESP.....
tr Q9AHT9 Q9AHT9_STRPN	EDP.....NKNFKA	DEEPVE..ET	P.AEP.....
tr Q8DQ08 Q8DQ08_STRR6	EKP.....EEDKEH	DEVSEP..TH	PESDEK.ENH	VGLNPS.ADN
tr Q9ANY2 Q9ANY2_STRPN	SKP.....DEDKEH	DEVSEP..TH	PESDEK.ENH	AGLNPS.ADN
tr Q9ANY3 Q9ANY3_STRPN	EKP.....SEEKPO	TEKPEE..ET	PREEKP.QSE	KPESP.....

tr Q8DQ07 Q8DQ07_STRR6	EEVPTVDPVQ	EKVAKFAESY	G.MKLENVLF	NMDGTIELYL	PSGEVIKKNM
tr Q6WNQ7 Q6WNQ7_STRPN	EEVPTVDPVQ	EKVAKFAESY	G.MKLENVLF	NMDGTIELYL	PSGEVIKKNM
tr Q9ANY1 Q9ANY1_STRPN	EEVPTVDPVQ	EKVAKFAESY	G.MKLENVLF	NMDGTIELYL	PSGEVIKKNM

tr Q6WNQ5 Q6WNQ5_STRPN	EEVPTVDPVQ	EKVAKFAESY	G.MKLENVLF	NMDGTIELYL	PSGEVIKKNM
tr Q8DPQ2 Q8DPQ2_STRR6E..VPQVET	...EKVEAQL	KEAEVLLAKV	
tr Q9AG74 Q9AG74_STRPN	..KPTEEP	ESPEESPE..	.ESEEPQVET	...EKVKEKL	REAEDLLGKI
tr Q9AHT9 Q9AHT9_STRPNE..VPQVET	...EKVEAQL	KEAEVLLAKV	
tr Q8DQ08 Q8DQ08_STRR6	LYKPSTDTEE	.TEEEAEDTT	DEAEIPQVEH	...SVINAKI	AEAEALLEKV
tr Q9ANY2 Q9ANY2_STRPN	LYKPSTDTEE	.TEEEAEDTT	DEAEIPQVEN	...SVINAKI	ADAEALLEKV
tr Q9ANY3 Q9ANY3_STRPN	..KPTEEP	.SPEESE..PQVET	...EKVEEKL	REAEDLLGKI

tr Q8DQ07 Q8DQ07_STRR6	ADFTGEAPQG	NGENKPSENG	KVSTGTVENQ	PTENKPADSL	PEAPNEKPVK
tr Q6WNQ7 Q6WNQ7_STRPN	ADFTGEAPQG	NGENKPSENG	KVSTGTVENQ	PTENKPADSL	PEAPNEKPVK
tr Q9ANY1 Q9ANY1_STRPN	ADFTGEAPQG	NGENKPSENG	KVSTGTVENQ	PTENKPADSL	PEAPNEKPVK
tr Q6WNQ5 Q6WNQ5_STRPN	ADFTGEAPQG	NGENKPSENG	KVSTGTVENQ	PTENKPADSL	PEAPNEKPVK
tr Q8DPQ2 Q8DPQ2_STRR6	TDSS..LKAN	ATETLAGLRN	NLTQLQIMDNN	.SIMAEAEKL	LALLKGS..N
tr Q9AG74 Q9AG74_STRPN	QNPI..IKSN	AKETLTGLKN	NLLFGTQDNN	.TIMAEAEKL	LALLKES..K
tr Q9AHT9 Q9AHT9_STRPN	TDSS..LKAN	ATETLAGLRN	NLTQLQIMDNN	.SIMAEAEKL	LALLKGS..N
tr Q8DQ08 Q8DQ08_STRR6	TDSS..IRQN	AVETLTGLKS	SLLLGTKDNN	.TISAEVDSL	LALLKES..Q
tr Q9ANY2 Q9ANY2_STRPN	TDPS..IRQN	AMETLTGLKS	SLLLGTKDNN	.TISAEVDSL	LALLKES..Q
tr Q9ANY3 Q9ANY3_STRPN	QDPI..IKSN	AKETLTGLKN	NLLFGTQDNN	.TIMAEAEKL	LALLKES..K

tr Q8DQ07 Q8DQ07_STRR6	PENSTDNGML	NPEGNVGSDP	MLDPALEEAP	AVDPVQEKLE	KFTASYGLGL
tr Q6WNQ7 Q6WNQ7_STRPN	PENSTDNGML	NPEGNVGSDP	MLDPALEEAP	AVDPVQEKLE	KFTASYGLGL
tr Q9ANY1 Q9ANY1_STRPN	PENSTDNGML	NPEGNVGSDP	MLDPALEEAP	AVDPVQEKLE	KFTASYGLGL
tr Q6WNQ5 Q6WNQ5_STRPN	PENSTDNGML	NPEGNVGSDP	MLDPALEEAP	AVDPVQEKLE	KFTASYGLGL
tr Q8DPQ2 Q8DPQ2_STRR6	PSSVSKEKIN
tr Q9AG74 Q9AG74_STRPN
tr Q9AHT9 Q9AHT9_STRPN	PSSVSKEKIN
tr Q8DQ08 Q8DQ08_STRR6	PTPIQ.....
tr Q9ANY2 Q9ANY2_STRPN	PAPIQ.....
tr Q9ANY3 Q9ANY3_STRPN

tr Q8DQ07 Q8DQ07_STRR6	DSVIFNMDGT	IELRLPSGEV	IKKNLSDLIA
tr Q6WNQ7 Q6WNQ7_STRPN	DSVIFNMDGT	IELRLPSGEV	IKKNLSDLIA
tr Q9ANY1 Q9ANY1_STRPN	DSVIFNMDGT	IELRLPSGEV	IKKNLSDLIA
tr Q6WNQ5 Q6WNQ5_STRPN	DSVIFNMDGT	IELRLPSGEV	IKKNLSDLIA
tr Q8DPQ2 Q8DPQ2_STRR6
tr Q9AG74 Q9AG74_STRPN
tr Q9AHT9 Q9AHT9_STRPN
tr Q8DQ08 Q8DQ08_STRR6
tr Q9ANY2 Q9ANY2_STRPN
tr Q9ANY3 Q9ANY3_STRPN

Alignments

tr Q8DQ07 *Pneumococcal histidine triad protein E [phtE] [Streptococcus pneumoniae (strain ATCC BAA-255 / R6)]* 1039 AA

align

Score = 2017 bits (5225), Expect = 0.0

Identities = 1004/1039 (96%), Positives = 1004/1039 (96%)

```
Query: 1   MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLTDPQVS 60
          MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLTDPQVS
Sbjct: 1   MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLTDPQVS 60

Query: 61  QKEGIQAEQIVIKITDQGYVTSHGDHYHYINGKVPYDALFSEELLMKDPNYQLKDADIVN 120
          QKEGIQAEQIVIKITDQGYVTSHGDHYHYINGKVPYDALFSEELLMKDPNYQLKDADIVN
Sbjct: 61  QKEGIQAEQIVIKITDQGYVTSHGDHYHYINGKVPYDALFSEELLMKDPNYQLKDADIVN 120

Query: 121 EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNNSNVAVARSQGRY 180
          EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNNSNVAVARSQGRY
Sbjct: 121 EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNNSNVAVARSQGRY 180

Query: 181 TTNDGYVFNPADIIEDTGNAYIVPHGGHYHYIPXXXXXXXXXXXXXXXXXXNMQPSQLS 240
          TTNDGYVFNPADIIEDTGNAYIVPHGGHYHYIP                                NMQPSQLS
Sbjct: 181 TTNDGYVFNPADIIEDTGNAYIVPHGGHYHYIPKSDLSASELAAAKAHLAGKNMQPSQLS 240

Query: 241 YSSTASDNNTQSVAKGSTSKPANKSENLSLLKELYDSPSAQRYSESDGLVFDPAKIISR 300
          YSSTASDNNTQSVAKGSTSKPANKSENLSLLKELYDSPSAQRYSESDGLVFDPAKIISR
Sbjct: 241 YSSTASDNNTQSVAKGSTSKPANKSENLSLLKELYDSPSAQRYSESDGLVFDPAKIISR 300

Query: 301 TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEVVXXXXXXXXXX 360
          TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEVV
Sbjct: 301 TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEVVSSLGSLSSN 360

Query: 361 XXXXXXXXKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA 420
          KELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA
Sbjct: 361 PSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA 420

Query: 421 TPSPSLPINPGISHEKHEEDGYGFDANRIIAEDES GFIMSHGNHNHYFFKKDLTEEQIKA 480
          TPSPSLPINPGISHEKHEEDGYGFDANRIIAEDES GFIMSHGNHNHYFFKKDLTEEQIKA
Sbjct: 421 TPSPSLPINPGISHEKHEEDGYGFDANRIIAEDES GFIMSHGNHNHYFFKKDLTEEQIKA 480

Query: 481 AQKHLEEVKTSHNGLDSLSSHEQDYPGNAKEMKDLDKKIEEKIAGIMKQYGVKRESIVVN 540
          AQKHLEEVKTSHNGLDSLSSHEQDYPGNAKEMKDLDKKIEEKIAGIMKQYGVKRESIVVN
Sbjct: 481 AQKHLEEVKTSHNGLDSLSSHEQDYPGNAKEMKDLDKKIEEKIAGIMKQYGVKRESIVVN 540

Query: 541 KEKNAI IYPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV 600
          KEKNAI IYPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV
Sbjct: 541 KEKNAI IYPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV 600

Query: 601 VNLLKNSTFNNQNFTLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVSQGVFG 660
          VNLLKNSTFNNQNFTLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVSQGVFG
Sbjct: 601 VNLLKNSTFNNQNFTLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVSQGVFG 660

Query: 661 EGVGNIANFELDQPYLPQGTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA 720
          EGVGNIANFELDQPYLPQGTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA
Sbjct: 661 EGVGNIANFELDQPYLPQGTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA 720
```


Query: 721 GDTYLRVNPQFAVPKGTDALVRVFDEFHGHNAYLENNYKVGEIKLPIPKLNQGTTRTAGNK 780
GDTYLRVNPQFAVPKGTDALVRVFDEFHGHNAYLENNYKVGEIKLPIPKLNQGTTRTAGNK
Sbjct: 721 GDTYLRVNPQFAVPKGTDALVRVFDEFHGHNAYLENNYKVGEIKLPIPKLNQGTTRTAGNK 780

Query: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS 840
IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS
Sbjct: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS 840

Query: 841 EKVEKEKLSETGNSTSNSTLEEVPTVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLP 900
EKVEKEKLSETGNSTSNSTLEEVPTVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLP
Sbjct: 841 EKVEKEKLSETGNSTSNSTLEEVPTVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLP 900

Query: 901 SGEVIKKNMADFTGEAPQNGENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960
SGEVIKKNMADFTGEAPQNGENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP
Sbjct: 901 SGEVIKKNMADFTGEAPQNGENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960

Query: 961 ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTI 1020
ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTI
Sbjct: 961 ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTI 1020

Query: 1021 ELRLPSGEVIKKNLSDLIA 1039
ELRLPSGEVIKKNLSDLIA
Sbjct: 1021 ELRLPSGEVIKKNLSDLIA 1039

tr Q6WNQ7 Surface protein BVH-3 [bvh-3] [Streptococcus 1039 AA
pneumoniae] align

Score = 2017 bits (5225), Expect = 0.0

Identities = 1004/1039 (96%), Positives = 1004/1039 (96%)

Query: 1 MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPQVS 60
MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPQVS
Sbjct: 1 MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPQVS 60

Query: 61 QKEGIQAEQIVIKITDQGYVTSHGHDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVN 120
QKEGIQAEQIVIKITDQGYVTSHGHDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVN
Sbjct: 61 QKEGIQAEQIVIKITDQGYVTSHGHDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVN 120

Query: 121 EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNSNVAVARSQGRY 180
EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNSNVAVARSQGRY
Sbjct: 121 EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNSNVAVARSQGRY 180

Query: 181 TTNDGYVFNPAIIEDTGNAYIVPHGGHYHYIPXXXXXXXXXXXXXXXXXXNMQPSQLS 240
TTNDGYVFNPAIIEDTGNAYIVPHGGHYHYIP NMQPSQLS
Sbjct: 181 TTNDGYVFNPAIIEDTGNAYIVPHGGHYHYIPKSDLSASELAAKAHLAKNMQPSQLS 240

Query: 241 YSSTASDNNTQSVAKGSTSKPANKSENLSLLKELYDPSAQRYSSES DGLVFDPAKIIISR 300
YSSTASDNNTQSVAKGSTSKPANKSENLSLLKELYDPSAQRYSSES DGLVFDPAKIIISR
Sbjct: 241 YSSTASDNNTQSVAKGSTSKPANKSENLSLLKELYDPSAQRYSSES DGLVFDPAKIIISR 300

Query: 301 TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEVVXXXXXXXXXX 360
TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEVV
Sbjct: 301 TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEVVSSLSLSSN 360

Query: 361 XXXXXXXKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA 420

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          KELSSASDGYIFNPKDIVEETATAYIVRHGDHPHYIPKSNQIGQPTLPNNSLA
Sbjct: 361 PSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHPHYIPKSNQIGQPTLPNNSLA 420

Query: 421 TPSPSLPINPGISHEKHEEDGYGFDANRIIAEDES GFIMSHGNHNYFFKKDLTEEQIKA 480
          TPSPSLPINPGISHEKHEEDGYGFDANRIIAEDES GFIMSHGNHNYFFKKDLTEEQIKA
Sbjct: 421 TPSPSLPINPGISHEKHEEDGYGFDANRIIAEDES GFIMSHGNHNYFFKKDLTEEQIKA 480

Query: 481 AQKHLEEVKTSNGLDLSLSHEQDYPGNAKEMKDLDDKKIEEKIAGIMKQYGVKRESIVVN 540
          AQKHLEEVKTSNGLDLSLSHEQDYPGNAKEMKDLDDKKIEEKIAGIMKQYGVKRESIVVN
Sbjct: 481 AQKHLEEVKTSNGLDLSLSHEQDYPGNAKEMKDLDDKKIEEKIAGIMKQYGVKRESIVVN 540

Query: 541 KEKNAIYYPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV 600
          KEKNAIYYPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV
Sbjct: 541 KEKNAIYYPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV 600

Query: 601 VNLLKNSTFNNQNFTLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVSQKVF 660
          VNLLKNSTFNNQNFTLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVSQKVF
Sbjct: 601 VNLLKNSTFNNQNFTLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVSQKVF 660

Query: 661 EGVGNIANFELDQPYLPGQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA 720
          EGVGNIANFELDQPYLPGQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA
Sbjct: 661 EGVGNIANFELDQPYLPGQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA 720

Query: 721 GDTYLRVNPQFAVPKGTDALVRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNK 780
          GDTYLRVNPQFAVPKGTDALVRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNK
Sbjct: 721 GDTYLRVNPQFAVPKGTDALVRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNK 780

Query: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS 840
          IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS
Sbjct: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS 840

Query: 841 EKVEKEKLSETGNSTSNSTLEEVPVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLP 900
          EKVEKEKLSETGNSTSNSTLEEVPVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLP
Sbjct: 841 EKVEKEKLSETGNSTSNSTLEEVPVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLP 900

Query: 901 SGEVIKKNMADFTGEAPQNGENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960
          SGEVIKKNMADFTGEAPQNGENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP
Sbjct: 901 SGEVIKKNMADFTGEAPQNGENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960

Query: 961 ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTI 1020
          ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTI
Sbjct: 961 ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTI 1020

Query: 1021 ELRLPSGEVIKKNLSDLIA 1039
          ELRLPSGEVIKKNLSDLIA
Sbjct: 1021 ELRLPSGEVIKKNLSDLIA 1039

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tr Q9ANY1 Pneumococcal histidine triad protein E precursor 1039
          (Hypothetical AA
          protein SP1004) [phtE] [Streptococcus pneumoniae] align

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Score = 2006 bits (5196), Expect = 0.0
Identities = 998/1039 (96%), Positives = 1000/1039 (96%)

Query: 1 MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPQVS 60

Sbjct: 1 MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPQVS 60
MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPQVS

Query: 61 QKEGIQAEQIVIKITDQGYVTSBGDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVN 120
QKEGIQAEQIVIKITDQGYVTSBGDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVN

Sbjct: 61 QKEGIQAEQIVIKITDQGYVTSBGDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVN 120

Query: 121 EVKGGYIIKVDGKYYVYLKDAHADNVRTKDEINRQKQEHVKDNEKVNNSNVAVARSQGRY 180
EVKGGYIIKVDGKYYVYLKDAHADNVRTKDEINRQKQEHVKDNEKVNNSNVAVARSQGRY

Sbjct: 121 EVKGGYIIKVDGKYYVYLKDAHADNVRTKDEINRQKQEHVKDNEKVNNSNVAVARSQGRY 180

Query: 181 TTNDGYVFNPAIIEDTGNAYIVPHGGHYHYIPXXXXXXXXXXXXXXXXXXXXNMQPSQLS 240
TTNDGYVFNPAIIEDTGNAYIVPHGGHYHYIP NMQPSQLS

Sbjct: 181 TTNDGYVFNPAIIEDTGNAYIVPHGGHYHYIPKSDLSASELAAAKAHLAKNMQPSQLS 240

Query: 241 YSSTASDNNTQSVAKGSTSKPANKSENLOSLKELYDSPAQRYSSESDGLVFDPAKIIISR 300
YSSTASDNNTQSVAKGSTSKPANKSENLOSLKELYDSPAQRYSSESDGLVFDPAKIIISR

Sbjct: 241 YSSTASDNNTQSVAKGSTSKPANKSENLOSLKELYDSPAQRYSSESDGLVFDPAKIIISR 300

Query: 301 TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEVXXXXXXXXXX 360
TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEV

Sbjct: 301 TPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPISGTGSTVSTNAKPNEVSSLGSLSSN 360

Query: 361 XXXXXXXXKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA 420
KELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA

Sbjct: 361 PSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA 420

Query: 421 TPSPSLPINPGISHEKHEEDGYGFDANRIIAEDES GFIMSHGNHNYFFKDLTEEQIKA 480
TPSPSLPINPG SHEKHEEDGYGFDANRIIAEDES GF+MSHG+HNHYFFKDLTEEQIKA

Sbjct: 421 TPSPSLPINPGTSHEKHEEDGYGFDANRIIAEDES GFVMSHGDNHNYFFKDLTEEQIKA 480

Query: 481 AQKHLEEVKTSHNGLDLSLSSHEQDYPGNAKEMKDLDDKKIEEKIAGIMKQYGVKRESIVN 540
AQKHLEEVKTSHNGLDLSLSSHEQDYP NAKEMKDLDDKKIEEKIAGIMKQYGVKRESIVN

Sbjct: 481 AQKHLEEVKTSHNGLDLSLSSHEQDYPNNAKEMKDLDDKKIEEKIAGIMKQYGVKRESIVN 540

Query: 541 KEKNAIIPYHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV 600
KEKNAIIPYHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV

Sbjct: 541 KEKNAIIPYHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV 600

Query: 601 VNLLKNSTFNNQNFLLANGQKRVSFSPPELEKKLGINMLVKLITPDGKVLEKVSQGVFG 660
VNLLKNSTFNNQNFLLANGQKRVSFSPPELEKKLGINMLVKLITPDGKVLEKVSQGVFG

Sbjct: 601 VNLLKNSTFNNQNFLLANGQKRVSFSPPELEKKLGINMLVKLITPDGKVLEKVSQGVFG 660

Query: 661 EGVGNIANFELDQPYLPGQTFKYTIASKDYEVSYDGTFTVPTSLAYKMASQTIFYPFHA 720
EGVGNIANFELDQPYLPGQTFKYTIASKDYEVSYDGTFTVPTSLAYKMASQTIFYPFHA

Sbjct: 661 EGVGNIANFELDQPYLPGQTFKYTIASKDYEVSYDGTFTVPTSLAYKMASQTIFYPFHA 720

Query: 721 GDTYLRVNPQFAVPKGTDALVRVDFEFHGNAYLENNYKVGEEKLPKLNQGTTRTAGNK 780
GDTYLRVNPQFAVPKGTDALVRVDFEFHGNAYLENNYKVGEEKLPKLNQGTTRTAGNK

Sbjct: 721 GDTYLRVNPQFAVPKGTDALVRVDFEFHGNAYLENNYKVGEEKLPKLNQGTTRTAGNK 780

Query: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS 840
IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQEN KLDEKVEEPKTS

Sbjct: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENLKLDEKVEEPKTS 840

Query: 841 EKVEKEKLSETGNSTSNSTLEEVPVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLP 900
EKVEKEKLSETGNSTSNSTLEEVPVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLP

Sbjct: 841 EKVEKEKLSETGNSTSNSTLEEVPVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLP 900

Query: 901 SGEVIKKNMADFTGEAPQGNGENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960
SGEVIKKNMADFTGEAPQGNGENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP
Sbjct: 901 SGEVIKKNMADFTGEAPQGNGENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960

Query: 961 ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTI 1020
ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTI
Sbjct: 961 ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTI 1020

Query: 1021 ELRLPSGEVIKKNLSDLIA 1039
ELRLPSGEVIKKNLSDLIA
Sbjct: 1021 ELRLPSGEVIKKNLSDLIA 1039

tr Q6WNQ5 Surface protein BVH-3 (Fragment) [bvh-3] [Streptococcus 1019
pneumoniae] AA
align

Score = 1968 bits (5099), Expect = 0.0

Identities = 977/1019 (95%), Positives = 979/1019 (95%)

Query: 21 CAYALNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPQVSQKEGIQAEQIVIKITDQGYV 80
CAYALNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPQVSQKEGIQAEQIVIKITDQGYV
Sbjct: 1 CAYALNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPQVSQKEGIQAEQIVIKITDQGYV 60

Query: 81 TSHGDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKD 140
TSHGDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKD
Sbjct: 61 TSHGDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKD 120

Query: 141 AAHADNVRTKDEINRQKQEHVKDNEKVNSNVAVARSQGRYTTNDGYVFNPAIIEDTGNA 200
AAHADNVRTKDEINRQKQEHVKDNEKVNSNVAVARSQGRYTTNDGYVFNPAIIEDTGNA
Sbjct: 121 AAHADNVRTKDEINRQKQEHVKDNEKVNSNVAVARSQGRYTTNDGYVFNPAIIEDTGNA 180

Query: 201 YIVPHGGHYHYIPXXXXXXXXXXXXXXXXXNMQPSQLSYSSTASDNNTQSVAKGSTSK 260
YIVPH GHYHYIP NMQPSQLSYSSTASDNNTQSVAKGSTSK
Sbjct: 181 YIVPHRGHYHYIPKSDLASASELAACAHLAGKNMQPSQLSYSSTASDNNTQSVAKGSTSK 240

Query: 261 PANKSENLSLLKELYDSPAQRYSSEDLGVFDPAKIISRTPNGVAIPHGDHYHFIPYSK 320
PANKSENLSLLKELYDSPAQRYSSEDLGVFDPAKIISRTPNGVAIPHGDHYHFIPYSK
Sbjct: 241 PANKSENLSLLKELYDSPAQRYSSEDLGVFDPAKIISRTPNGVAIPHGDHYHFIPYSK 300

Query: 321 LSALEEKIARRVPISGTGSTVSTNAKPNEVVXXXXXXXXXXXXXXXXXKELSSASDGYIFN 380
LSALEEKIAR VPISGTGSTVSTNAKPNEVV KELSSASDGYIFN
Sbjct: 301 LSALEEKIARMVPISGTGSTVSTNAKPNEVVSLGSLSSNPSSLTTSKELSSASDGYIFN 360

Query: 381 PKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLATPSPSLPINPGISHEKHEED 440
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          (strain ATCC BAA-255 / R6)]      align

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Score = 442 bits (1137), Expect = e-122

Identities = 219/369 (59%), Positives = 271/369 (73%), Gaps = 21/369 (5%)

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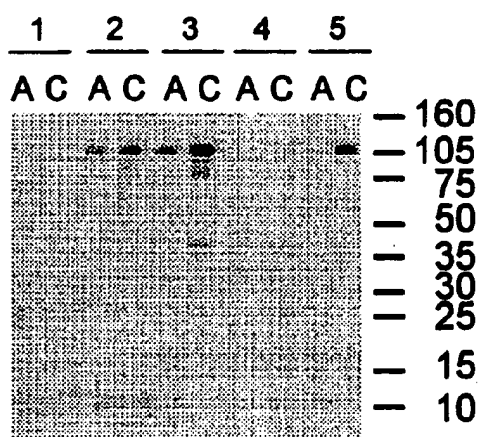
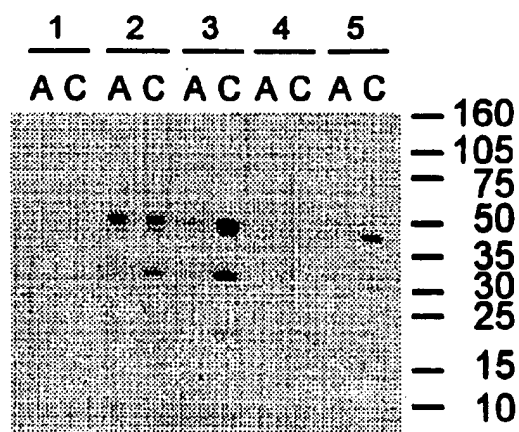
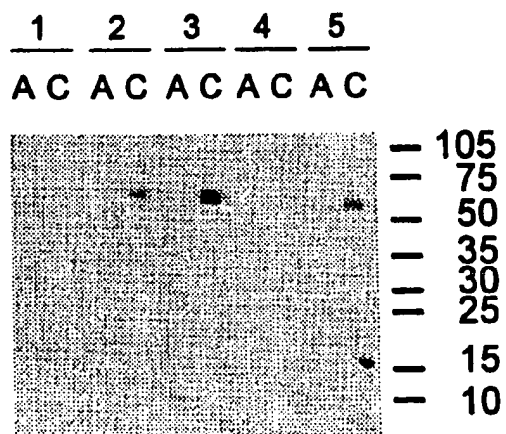
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           + + E G I A E Q I V I K I T D Q G Y V T S H G D H Y H Y N G K V P Y D A + S E E L L M K D P N Y Q L K D D I + +
Sbjct: 71  K R E G I N A E Q I V I K I T D Q G Y V T S H G D H Y H Y N G K V P Y D A I I S E E L L M K D P N Y Q L K D E D I I S 130

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```

Figure 5**A. Full-length Sp36****B. N-terminus****C. C-terminus**

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UniProtKB/TrEMBL

entry Q9ANY1

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[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information


Entry name	Q9ANY1_STRPN
Primary accession number	Q9ANY1
Secondary accession number	Q7D4B6
Entered in TrEMBL in	Release 17, June 2001
Sequence was last modified in	Release 17, June 2001
Annotations were last modified in	Release 30, May 2005
Name and origin of the protein	
Protein name	Pneumococcal histidine triad protein E [Precursor]
Synonym	Hypothetical protein SP1004
Gene name	Name: phtE
	OrderedLocusNames: SP1004
From	Streptococcus pneumoniae [TaxID: 1313]
Taxonomy	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.

References

[1] NUCLEOTIDE SEQUENCE.

DOI=10.1128/IAI.69.2.949-958.2001; PubMed=11159990 [NCBI, ExPASy, EBI, Israel, Japan]
 Adamou J.E., Heinrichs J.H., Erwin A.L., Walsh W., Gayle T., Dormitzer M., Dagan R., Brewah
 Y.A., Barren P., Lathigra R., Langermann S., Koenig S., Johnson S.;
 "Identification and characterization of a novel family of pneumococcal proteins (the Pht family) that
 are protective against sepsis.";
 Infect. Immun. 69:949-958(2001).

[2] NUCLEOTIDE SEQUENCE.

STRAIN=ATCC BAA-334 / TIGR4;
 DOI=10.1126/science.1061217; PubMed=11463916 [NCBI, ExPASy, EBI, Israel, Japan]
 Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S.N., Heidelberg J.F., DeBoy
 R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M.L., Kolonay J.F., Nelson W.C., Peterson J.D.,
 Umayam L.A., White O., Salzberg S.L., Lewis M.R., , Fraser C.M.;
 "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.";
 Science 293:498-506(2001).

Comments

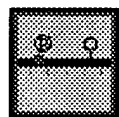
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Cross-references

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[EMBL / GenBank / DDBJ]
 [CoDingSequence]

EMBL AE007403; AAK75121.1; -; [EMBL / GenBank / DDBJ]
 Genomic_DNA. [CoDingSequence]
 PIR H95115; H95115.
 TIGR SP1004; -.
 InterPro IPR006270; Strep_his_triad.
 Graphical view of domain structure.
 Pfam PF04270; Strep_his_triad; 5.
 Pfam graphical view of domain structure.
 TIGRFAMs TIGR01363; strep_his_triad; 3.
 ProDom [Domain structure / List of seq. sharing at least 1 domain]
 HOGENOM [Family / Alignment / Tree]
 ProtoMap Q9ANY1.
 PRESAGE Q9ANY1.
 ModBase Q9ANY1.
 SWISS-2DPAGE Get region on 2D PAGE.
 UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords**Complete proteome; Hypothetical protein; Signal.****Features**

Feature table viewer

Key	From	To	Length	Description
SIGNAL	1	29	29	Potential.

Sequence information

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<u>130</u>	<u>140</u>	<u>150</u>	<u>160</u>	<u>170</u>	<u>180</u>
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<u>190</u>	<u>200</u>	<u>210</u>	<u>220</u>	<u>230</u>	<u>240</u>
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<u>310</u>	<u>320</u>	<u>330</u>	<u>340</u>	<u>350</u>	<u>360</u>
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      550      560      570      580      590      600
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      850      860      870      880      890      900
EKVEKEKLSE TGNSTSNSTL EEVPTVDPVQ EKVAKFAESY GMKLENVLFN MDGTIELYLP
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SGEVIKKNMA DFTGEAPQGN GENKPSENGK VSTGTVENQP TENKPADSLP EAPNEKPVKP
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Q9ANY1 in FASTA
format

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View entry in raw text format (no links)

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BLAST

BLAST submission on
ExPASy/SIB
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)



ScanProsite, MotifScan



Submit a homology modeling request to SWISS-
MODEL



NPSA Sequence analysis
tools



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tr Q9ANY1 **Pneumococcal histidine triad protein E precursor** 1039
 Q9ANY1_STRPN **(Hypothetical** AA
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Score = 2006 bits (5196), Expect = 0.0

Identities = 998/1039 (96%), Positives = 1000/1039 (96%)

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tr Q8DQ07 **Pneumococcal histidine triad protein E [phtE]** 1039
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Query: 61      QKEGIQAEQIVIKITDQGYVTSHGDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVN 120
              QKEGIQAEQIVIKITDQGYVTSHGDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVN
Sbjct: 61      QKEGIQAEQIVIKITDQGYVTSHGDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVN 120

Query: 121     EVKGGYIIKVDGKYVYVLKDAAHADNVRTKDEINRQKQEHVKDNEKVNNSNVAVARSQGRY 180
              EVKGGYIIKVDGKYVYVLKDAAHADNVRTKDEINRQKQEHVKDNEKVNNSNVAVARSQGRY
Sbjct: 121     EVKGGYIIKVDGKYVYVLKDAAHADNVRTKDEINRQKQEHVKDNEKVNNSNVAVARSQGRY 180

Query: 181     TTNDGYVFNPAIIEDTGNAYIVPHGGHYHYIPXXXXXXXXXXXXXXXXXXNMQPSQLS 240
              TTNDGYVFNPAIIEDTGNAYIVPHGGHYHYIP                                NMQPSQLS
Sbjct: 181     TTNDGYVFNPAIIEDTGNAYIVPHGGHYHYIPKSDLSASELAAKAHLAKNMQPSQLS 240

Query: 241     YSSTASDNNTQSVAKGSTSKPANKSENLSLLKELYDSPSAQRYSESDGLVFDPAKIIISR 300
              YSSTASDNNTQSVAKGSTSKPANKSENLSLLKELYDSPSAQRYSESDGLVFDPAKIIISR
Sbjct: 241     YSSTASDNNTQSVAKGSTSKPANKSENLSLLKELYDSPSAQRYSESDGLVFDPAKIIISR 300

Query: 301     TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEVXXXXXXXXXX 360
              TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEV
Sbjct: 301     TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEVSSLGSLSSN 360

Query: 361     XXXXXXXXKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA 420
              KELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA
Sbjct: 361     PSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA 420

Query: 421     TPSPSLPINPGISHEKHEEDGYGFDANRIIAEDES GFIMSHGNHNHYFFKKDLTEEQIKA 480
              TPSPSLPINPGISHEKHEEDGYGFDANRIIAEDES GFIMSHGNHNHYFFKKDLTEEQIKA
Sbjct: 421     TPSPSLPINPGISHEKHEEDGYGFDANRIIAEDES GFIMSHGNHNHYFFKKDLTEEQIKA 480

Query: 481     AQKHLEEVKTS HNGLDLSLSHEQDYPGNAKEMKDLDKKIEEKIAGIMKQYGVKRESIVVN 540
              AQKHLEEVKTS HNGLDLSLSHEQDYPGNAKEMKDLDKKIEEKIAGIMKQYGVKRESIVVN
Sbjct: 481     AQKHLEEVKTS HNGLDLSLSHEQDYPGNAKEMKDLDKKIEEKIAGIMKQYGVKRESIVVN 540

Query: 541     KEKNAIIPYPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV 600
              KEKNAIIPYPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV
Sbjct: 541     KEKNAIIPYPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV 600

Query: 601     VNLLKNSTFNNQNF TLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVS GKVFG 660
              VNLLKNSTFNNQNF TLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVS GKVFG
Sbjct: 601     VNLLKNSTFNNQNF TLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKVLEKVS GKVFG 660

Query: 661     EGVGNIANFELDQPYLPQGTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTI FYPFHA 720
              EGVGNIANFELDQPYLPQGTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTI FYPFHA
Sbjct: 661     EGVGNIANFELDQPYLPQGTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTI FYPFHA 720

Query: 721     GDTYLRVNPQFAVPKGT DALVRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNK 780
              GDTYLRVNPQFAVPKGT DALVRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNK
Sbjct: 721     GDTYLRVNPQFAVPKGT DALVRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNK 780

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Query: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS 840
IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS
Sbjct: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS 840

Query: 841 EKVEKEKLSETGNSTSNSTLEEVPTVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLP 900
EKVEKEKLSETGNSTSNSTLEEVPTVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLP
Sbjct: 841 EKVEKEKLSETGNSTSNSTLEEVPTVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLP 900

Query: 901 SGEVIKKNMADFTGEAPQGNGENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960
SGEVIKKNMADFTGEAPQGNGENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP
Sbjct: 901 SGEVIKKNMADFTGEAPQGNGENKPSSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960

Query: 961 ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTI 1020
ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTI
Sbjct: 961 ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTI 1020

Query: 1021 ELRLPSGEVIKKNLSDLIA 1039
ELRLPSGEVIKKNLSDLIA
Sbjct: 1021 ELRLPSGEVIKKNLSDLIA 1039

CLUSTAL W (1.74) multiple sequence alignment

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tr|Q9ANY1|Q9ANY1_STRPN      MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNRRVSYVDGSQSSQK
tr|Q8DQ07|Q8DQ07_STRR6      MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNRRVSYVDGSQSSQK
tr|Q6WNQ7|Q6WNQ7_STRPN      MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNRRVSYVDGSQSSQK
tr|Q6WNQ5|Q6WNQ5_STRPN      -----CAYALNQHRSQENKDNRRVSYVDGSQSSQK
                               *****

tr|Q9ANY1|Q9ANY1_STRPN      SENLTPDQVSQKEGIQAEQIVIKITDQGYVTSHGDHYHYNGKVPYDALF
tr|Q8DQ07|Q8DQ07_STRR6      SENLTPDQVSQKEGIQAEQIVIKITDQGYVTSHGDHYHYNGKVPYDALF
tr|Q6WNQ7|Q6WNQ7_STRPN      SENLTPDQVSQKEGIQAEQIVIKITDQGYVTSHGDHYHYNGKVPYDALF
tr|Q6WNQ5|Q6WNQ5_STRPN      SENLTPDQVSQKEGIQAEQIVIKITDQGYVTSHGDHYHYNGKVPYDALF
                               *****

tr|Q9ANY1|Q9ANY1_STRPN      SEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKDAAHADNVRTK
tr|Q8DQ07|Q8DQ07_STRR6      SEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKDAAHADNVRTK
tr|Q6WNQ7|Q6WNQ7_STRPN      SEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKDAAHADNVRTK
tr|Q6WNQ5|Q6WNQ5_STRPN      SEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKDAAHADNVRTK
                               *****

tr|Q9ANY1|Q9ANY1_STRPN      DEINRQKQEHVKDNEKVNNSVAVARSQGRYTTNDGYVFNPAIIEDTGNA
tr|Q8DQ07|Q8DQ07_STRR6      DEINRQKQEHVKDNEKVNNSVAVARSQGRYTTNDGYVFNPAIIEDTGNA
tr|Q6WNQ7|Q6WNQ7_STRPN      DEINRQKQEHVKDNEKVNNSVAVARSQGRYTTNDGYVFNPAIIEDTGNA
tr|Q6WNQ5|Q6WNQ5_STRPN      DEINRQKQEHVKDNEKVNNSVAVARSQGRYTTNDGYVFNPAIIEDTGNA
                               *****

tr|Q9ANY1|Q9ANY1_STRPN      YIVPHGGHYHYI PKSDLSASELAAKAHLAGKNMQPSQLSYSSTASDNNT
tr|Q8DQ07|Q8DQ07_STRR6      YIVPHGGHYHYI PKSDLSASELAAKAHLAGKNMQPSQLSYSSTASDNNT
tr|Q6WNQ7|Q6WNQ7_STRPN      YIVPHGGHYHYI PKSDLSASELAAKAHLAGKNMQPSQLSYSSTASDNNT
tr|Q6WNQ5|Q6WNQ5_STRPN      YIVPHRGHYHYI PKSDLSASELAAKAHLAGKNMQPSQLSYSSTASDNNT
                               *****

tr|Q9ANY1|Q9ANY1_STRPN      QSVAKGSTSKPANKSENLSLLKELYDSPSAQRYSESDGLVFDPAKIIISR
tr|Q8DQ07|Q8DQ07_STRR6      QSVAKGSTSKPANKSENLSLLKELYDSPSAQRYSESDGLVFDPAKIIISR
tr|Q6WNQ7|Q6WNQ7_STRPN      QSVAKGSTSKPANKSENLSLLKELYDSPSAQRYSESDGLVFDPAKIIISR
tr|Q6WNQ5|Q6WNQ5_STRPN      QSVAKGSTSKPANKSENLSLLKELYDSPSAQRYSESDGLVFDPAKIIISR
                               *****

tr|Q9ANY1|Q9ANY1_STRPN      TPNGVAIPHGDHYHFI PYSKLSALEEKIARMVPISGTGSTVSTNAKPNEV
tr|Q8DQ07|Q8DQ07_STRR6      TPNGVAIPHGDHYHFI PYSKLSALEEKIARRVPISGTGSTVSTNAKPNEV
tr|Q6WNQ7|Q6WNQ7_STRPN      TPNGVAIPHGDHYHFI PYSKLSALEEKIARRVPISGTGSTVSTNAKPNEV
tr|Q6WNQ5|Q6WNQ5_STRPN      TPNGVAIPHGDHYHFI PYSKLSALEEKIARMVPISGTGSTVSTNAKPNEV
                               *****

tr|Q9ANY1|Q9ANY1_STRPN      VSSLGSLSSNPSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHF
tr|Q8DQ07|Q8DQ07_STRR6      VSSLGSLSSNPSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHF
tr|Q6WNQ7|Q6WNQ7_STRPN      VSSLGSLSSNPSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHF
tr|Q6WNQ5|Q6WNQ5_STRPN      VSSLGSLSSNPSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHF
                               *****

tr|Q9ANY1|Q9ANY1_STRPN      HYIPKSNQIGQPTLPNNSLATPSPSLPINPGTSHEKHEEDGYGFDANRII
tr|Q8DQ07|Q8DQ07_STRR6      HYIPKSNQIGQPTLPNNSLATPSPSLPINPGISHEKHEEDGYGFDANRII
tr|Q6WNQ7|Q6WNQ7_STRPN      HYIPKSNQIGQPTLPNNSLATPSPSLPINPGISHEKHEEDGYGFDANRII
tr|Q6WNQ5|Q6WNQ5_STRPN      HYIPKSNQIGQPTLPNNSLATPSPSLPINPGTSHEKHEEDGYGFDANRII
                               *****

tr|Q9ANY1|Q9ANY1_STRPN      AEDESGFVMSHGDNHNYFFKKDLTEEQIKAAQKHLEEVKTSHNGLDSLSS
tr|Q8DQ07|Q8DQ07_STRR6      AEDESGFIMSHGNHNYFFKKDLTEEQIKAAQKHLEEVKTSHNGLDSLSS
tr|Q6WNQ7|Q6WNQ7_STRPN      AEDESGFIMSHGNHNYFFKKDLTEEQIKAAQKHLEEVKTSHNGLDSLSS

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tr Q6WNQ5 Q6WNQ5_STRPN	AEDESGFVMSHGDHNNHYFFKKDLTEEQIKAAQKHLEEVKTSNGLDSLSS *****:*****:*****
tr Q9ANY1 Q9ANY1_STRPN	HEQDYPSNAKEMKDLDDKKIEEKIAGIMKQYGVKRESIVVNKEKNAIYYPH
tr Q8DQ07 Q8DQ07_STRR6	HEQDYPGNAKEMKDLDDKKIEEKIAGIMKQYGVKRESIVVNKEKNAIYYPH
tr Q6WNQ7 Q6WNQ7_STRPN	HEQDYPSNAKEMKDLDDKKIEEKIAGIMKQYGVKRESIVVNKEKNAIYYPH
tr Q6WNQ5 Q6WNQ5_STRPN	HEQDYPSNAKEMKDLDDKKIEEKIAGIMKQYGVKRESIVVNKEKNAIYYPH *****:*****:*****
tr Q9ANY1 Q9ANY1_STRPN	GDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGKVKYTGEELTNV
tr Q8DQ07 Q8DQ07_STRR6	GDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGKVKYTGEELTNV
tr Q6WNQ7 Q6WNQ7_STRPN	GDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGKVKYTGEELTNV
tr Q6WNQ5 Q6WNQ5_STRPN	GDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGKVKYTGEELTNV *****:*****:*****
tr Q9ANY1 Q9ANY1_STRPN	VNLLKNSTFNNQNFNFTLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKV
tr Q8DQ07 Q8DQ07_STRR6	VNLLKNSTFNNQNFNFTLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKV
tr Q6WNQ7 Q6WNQ7_STRPN	VNLLKNSTFNNQNFNFTLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKV
tr Q6WNQ5 Q6WNQ5_STRPN	VNLLKNSTFNNQNFNFTLANGQKRVSFSFPPELEKKLGINMLVKLITPDGKV *****:*****:*****
tr Q9ANY1 Q9ANY1_STRPN	LEKVSQKVFGEVGNIANFELDQPYLPGQTFKYTIASKDYPEVSYDGTFT
tr Q8DQ07 Q8DQ07_STRR6	LEKVSQKVFGEVGNIANFELDQPYLPGQTFKYTIASKDYPEVSYDGTFT
tr Q6WNQ7 Q6WNQ7_STRPN	LEKVSQKVFGEVGNIANFELDQPYLPGQTFKYTIASKDYPEVSYDGTFT
tr Q6WNQ5 Q6WNQ5_STRPN	LEKVSQKVFGEVGNIANFELDQPYLPGQTFKYTIASKDYPEVSYDGTFT *****:*****:*****
tr Q9ANY1 Q9ANY1_STRPN	VPTSLAYKMASQTI FYPFHAGDTYLRVNPQFAVPKGTDALVRVFDEFHGN
tr Q8DQ07 Q8DQ07_STRR6	VPTSLAYKMASQTI FYPFHAGDTYLRVNPQFAVPKGTDALVRVFDEFHGN
tr Q6WNQ7 Q6WNQ7_STRPN	VPTSLAYKMASQTI FYPFHAGDTYLRVNPQFAVPKGTDALVRVFDEFHGN
tr Q6WNQ5 Q6WNQ5_STRPN	VPTSLAYKMASQTI FYPFHAGDTYLRVNPQFAVPKGTDALVRVFDEFHGN *****:*****:*****
tr Q9ANY1 Q9ANY1_STRPN	AYLENNYKVGEIKLPIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVE
tr Q8DQ07 Q8DQ07_STRR6	AYLENNYKVGEIKLPIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVE
tr Q6WNQ7 Q6WNQ7_STRPN	AYLENNYKVGEIKLPIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVE
tr Q6WNQ5 Q6WNQ5_STRPN	AYLENNYKVGEIKLPIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVE *****:*****:*****
tr Q9ANY1 Q9ANY1_STRPN	VPILEKENQTDKPSILPQFKNKAQENLKLDEKVEEPKTSEKVEKEKLSE
tr Q8DQ07 Q8DQ07_STRR6	VPILEKENQTDKPSILPQFKNKAQENLKLDEKVEEPKTSEKVEKEKLSE
tr Q6WNQ7 Q6WNQ7_STRPN	VPILEKENQTDKPSILPQFKNKAQENLKLDEKVEEPKTSEKVEKEKLSE
tr Q6WNQ5 Q6WNQ5_STRPN	VPILEKENQTDKPSILPQFKNKAQENLKLDEKVEEPKTSEKVEKEKLSE *****:*****:*****
tr Q9ANY1 Q9ANY1_STRPN	TGNSTSNSTLEEVPVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLP
tr Q8DQ07 Q8DQ07_STRR6	TGNSTSNSTLEEVPVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLP
tr Q6WNQ7 Q6WNQ7_STRPN	TGNSTSNSTLEEVPVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLP
tr Q6WNQ5 Q6WNQ5_STRPN	TGNSTSNSTLEEVPVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLP *****:*****:*****
tr Q9ANY1 Q9ANY1_STRPN	SGEVIKKNMADFTGEAPQGNGENKPSSENGKVSTGTVENQPTENKPADSLP
tr Q8DQ07 Q8DQ07_STRR6	SGEVIKKNMADFTGEAPQGNGENKPSSENGKVSTGTVENQPTENKPADSLP
tr Q6WNQ7 Q6WNQ7_STRPN	SGEVIKKNMADFTGEAPQGNGENKPSSENGKVSTGTVENQPTENKPADSLP
tr Q6WNQ5 Q6WNQ5_STRPN	SGEVIKKNMADFTGEAPQGNGENKPSSENGKVSTGTVENQPTENKPADSLP *****:*****:*****
tr Q9ANY1 Q9ANY1_STRPN	EAPNEKPVKPENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEK
tr Q8DQ07 Q8DQ07_STRR6	EAPNEKPVKPENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEK
tr Q6WNQ7 Q6WNQ7_STRPN	EAPNEKPVKPENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEK

tr Q6WNQ5 Q6WNQ5_STRPN	EAPNEKPVKPENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEK *****
tr Q9ANY1 Q9ANY1_STRPN	FTASYGLGLDSVIFNMDGTIELRLPSGEVIKKNLSDLIA
tr Q8DQ07 Q8DQ07_STRR6	FTASYGLGLDSVIFNMDGTIELRLPSGEVIKKNLSDLIA
tr Q6WNQ7 Q6WNQ7_STRPN	FTASYGLGLDSVIFNMDGTIELRLPSGEVIKKNLSDLIA
tr Q6WNQ5 Q6WNQ5_STRPN	FTASYGLGLDSVIFNMDGTIELRLPSGEVIKKNLSDLIA *****

FileUp

MSF: 1039 Type: P Check: 304 ..

Name: tr|Q9ANY1|Q9ANY1_STRPN oo Len: 1039 Check: 9358 Weight: 0.100
 Name: tr|Q8DQ07|Q8DQ07_STRR6 oo Len: 1039 Check: 8867 Weight: 0.100
 Name: tr|Q6WNQ7|Q6WNQ7_STRPN oo Len: 1039 Check: 8867 Weight: 0.100
 Name: tr|Q6WNQ5|Q6WNQ5_STRPN oo Len: 1039 Check: 3212 Weight: 0.100

//

tr Q9ANY1 Q9ANY1_STRPN	MKFSKKYIAA	GSAVIVSLSL	CAYALNQHRS	QENKDNRRVS	YVDGSQSSQK
tr Q8DQ07 Q8DQ07_STRR6	MKFSKKYIAA	GSAVIVSLSL	CAYALNQHRS	QENKDNRRVS	YVDGSQSSQK
tr Q6WNQ7 Q6WNQ7_STRPN	MKFSKKYIAA	GSAVIVSLSL	CAYALNQHRS	QENKDNRRVS	YVDGSQSSQK
tr Q6WNQ5 Q6WNQ5_STRPN	CAYALNQHRS	QENKDNRRVS	YVDGSQSSQK

tr Q9ANY1 Q9ANY1_STRPN	SENLTDPQVS	QKEGIQAEQI	VIKITDQGYV	TSHGDHYHYY	NGKVPYDALF
tr Q8DQ07 Q8DQ07_STRR6	SENLTDPQVS	QKEGIQAEQI	VIKITDQGYV	TSHGDHYHYY	NGKVPYDALF
tr Q6WNQ7 Q6WNQ7_STRPN	SENLTDPQVS	QKEGIQAEQI	VIKITDQGYV	TSHGDHYHYY	NGKVPYDALF
tr Q6WNQ5 Q6WNQ5_STRPN	SENLTDPQVS	QKEGIQAEQI	VIKITDQGYV	TSHGDHYHYY	NGKVPYDALF

tr Q9ANY1 Q9ANY1_STRPN	SEELLMKDPN	YQLKDADIVN	EVKGGYIIKV	DGKYYVYLKD	AAHADNVRTK
tr Q8DQ07 Q8DQ07_STRR6	SEELLMKDPN	YQLKDADIVN	EVKGGYIIKV	DGKYYVYLKD	AAHADNVRTK
tr Q6WNQ7 Q6WNQ7_STRPN	SEELLMKDPN	YQLKDADIVN	EVKGGYIIKV	DGKYYVYLKD	AAHADNVRTK
tr Q6WNQ5 Q6WNQ5_STRPN	SEELLMKDPN	YQLKDADIVN	EVKGGYIIKV	DGKYYVYLKD	AAHADNVRTK

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tr Q8DQ07 Q8DQ07_STRR6	DEINRQKQEH	VKDNEKVNSN	VAVARSQGRY	TTNDGYVFNP	ADIIEDTGNA
tr Q6WNQ7 Q6WNQ7_STRPN	DEINRQKQEH	VKDNEKVNSN	VAVARSQGRY	TTNDGYVFNP	ADIIEDTGNA
tr Q6WNQ5 Q6WNQ5_STRPN	DEINRQKQEH	VKDNEKVNSN	VAVARSQGRY	TTNDGYVFNP	ADIIEDTGNA

tr Q9ANY1 Q9ANY1_STRPN	YIVPHGGHYH	YIPKSDLSAS	ELAAAKAHLA	GKNMQPSQLS	YSSTASDNNT
tr Q8DQ07 Q8DQ07_STRR6	YIVPHGGHYH	YIPKSDLSAS	ELAAAKAHLA	GKNMQPSQLS	YSSTASDNNT
tr Q6WNQ7 Q6WNQ7_STRPN	YIVPHGGHYH	YIPKSDLSAS	ELAAAKAHLA	GKNMQPSQLS	YSSTASDNNT
tr Q6WNQ5 Q6WNQ5_STRPN	YIVPHRGHYH	YIPKSDLSAS	ELAAAKAHLA	GKNMQPSQLS	YSSTASDNNT

tr Q9ANY1 Q9ANY1_STRPN	QSVAKGSTSK	PANKSENLOS	LLKELYDSPS	AQRYSESDGL	VFDPAKIISR
tr Q8DQ07 Q8DQ07_STRR6	QSVAKGSTSK	PANKSENLOS	LLKELYDSPS	AQRYSESDGL	VFDPAKIISR
tr Q6WNQ7 Q6WNQ7_STRPN	QSVAKGSTSK	PANKSENLOS	LLKELYDSPS	AQRYSESDGL	VFDPAKIISR
tr Q6WNQ5 Q6WNQ5_STRPN	QSVAKGSTSK	PANKSENLOS	LLKELYDSPS	AQRYSESDGL	VFDPAKIISR

tr Q9ANY1 Q9ANY1_STRPN	TPNGVAIPHG	DHYHFIPYSK	LSALEEKIAR	MVPISGTGST	VSTNAKPNEV
tr Q8DQ07 Q8DQ07_STRR6	TPNGVAIPHG	DHYHFIPYSK	LSALEEKIAR	RVPISTGTGST	VSTNAKPNEV
tr Q6WNQ7 Q6WNQ7_STRPN	TPNGVAIPHG	DHYHFIPYSK	LSALEEKIAR	RVPISTGTGST	VSTNAKPNEV
tr Q6WNQ5 Q6WNQ5_STRPN	TPNGVAIPHG	DHYHFIPYSK	LSALEEKIAR	MVPISGTGST	VSTNAKPNEV

tr Q9ANY1 Q9ANY1_STRPN	VSSLGSLSSN	PSSLTTSKEL	SSASDGYIFN	PKDIVEETAT	AYIVRHGDHF
tr Q8DQ07 Q8DQ07_STRR6	VSSLGSLSSN	PSSLTTSKEL	SSASDGYIFN	PKDIVEETAT	AYIVRHGDHF
tr Q6WNQ7 Q6WNQ7_STRPN	VSSLGSLSSN	PSSLTTSKEL	SSASDGYIFN	PKDIVEETAT	AYIVRHGDHF

tr Q6WNQ5 Q6WNQ5_STRPN	VSSLGSLSSN PSSLTTSKEL SSASDGYIFN PKDIVEETAT AYIVRHGDHF
tr Q9ANY1 Q9ANY1_STRPN	HYIPKSNQIG QPTLPNNSLA TPSPSLPINP GTSHEKHEED GYGFDANRII
tr Q8DQ07 Q8DQ07_STRR6	HYIPKSNQIG QPTLPNNSLA TPSPSLPINP GISHEKHEED GYGFDANRII
tr Q6WNQ7 Q6WNQ7_STRPN	HYIPKSNQIG QPTLPNNSLA TPSPSLPINP GISHEKHEED GYGFDANRII
tr Q6WNQ5 Q6WNQ5_STRPN	HYIPKSNQIG QPTLPNNSLA TPSPSLPINP GTSHEKHEED GYGFDANRII
tr Q9ANY1 Q9ANY1_STRPN	AEDESGFVMS HGDHNHYFFK KDLTEEQIKA AQKHLEEVKT SHNGLDSLSS
tr Q8DQ07 Q8DQ07_STRR6	AEDESGFIMS HGNHNHYFFK KDLTEEQIKA AQKHLEEVKT SHNGLDSLSS
tr Q6WNQ7 Q6WNQ7_STRPN	AEDESGFIMS HGNHNHYFFK KDLTEEQIKA AQKHLEEVKT SHNGLDSLSS
tr Q6WNQ5 Q6WNQ5_STRPN	AEDESGFVMS HGDHNHYFFK KDLTEEQIKA AQKHLEEVKT SHNGLDSLSS
tr Q9ANY1 Q9ANY1_STRPN	HEQDYPSSNAK EMKDLDDKKIE EKIAGIMKQY GVKRESIVVN KEKNAIYYPH
tr Q8DQ07 Q8DQ07_STRR6	HEQDYPGNAK EMKDLDDKKIE EKIAGIMKQY GVKRESIVVN KEKNAIYYPH
tr Q6WNQ7 Q6WNQ7_STRPN	HEQDYPGNAK EMKDLDDKKIE EKIAGIMKQY GVKRESIVVN KEKNAIYYPH
tr Q6WNQ5 Q6WNQ5_STRPN	HEQDYPSSNAK EMKDLDDKKIE EKIAGIMKQY GVKRESIVVN KEKNAIYYPH
tr Q9ANY1 Q9ANY1_STRPN	GDHHHADPID EHHPVGIGHS HSNYELFKPE EGVAKKEGNK VYTGEELTNV
tr Q8DQ07 Q8DQ07_STRR6	GDHHHADPID EHHPVGIGHS HSNYELFKPE EGVAKKEGNK VYTGEELTNV
tr Q6WNQ7 Q6WNQ7_STRPN	GDHHHADPID EHHPVGIGHS HSNYELFKPE EGVAKKEGNK VYTGEELTNV
tr Q6WNQ5 Q6WNQ5_STRPN	GDHHHADPID EHHPVGIGHS HSNYELFKPE EGVAKKEGNK VYTGEELTNV
tr Q9ANY1 Q9ANY1_STRPN	VNLLKNSTFN NQNFTLANGQ KRVSFSFPPE LEKKLGINML VKLITPDGKV
tr Q8DQ07 Q8DQ07_STRR6	VNLLKNSTFN NQNFTLANGQ KRVSFSFPPE LEKKLGINML VKLITPDGKV
tr Q6WNQ7 Q6WNQ7_STRPN	VNLLKNSTFN NQNFTLANGQ KRVSFSFPPE LEKKLGINML VKLITPDGKV
tr Q6WNQ5 Q6WNQ5_STRPN	VNLLKNSTFN NQNFTLANGQ KRVSFSFPPE LEKKLGINML VKLITPDGKV
tr Q9ANY1 Q9ANY1_STRPN	LEKVSGKVFG EGVGNIANFE LDQPYLPGQT FKYTIASKDY PEVSYDGTFT
tr Q8DQ07 Q8DQ07_STRR6	LEKVSGKVFG EGVGNIANFE LDQPYLPGQT FKYTIASKDY PEVSYDGTFT
tr Q6WNQ7 Q6WNQ7_STRPN	LEKVSGKVFG EGVGNIANFE LDQPYLPGQT FKYTIASKDY PEVSYDGTFT
tr Q6WNQ5 Q6WNQ5_STRPN	LEKVSGKVFG EGVGNIANFE LDQPYLPGQT FKYTIASKDY PEVSYDGTFT
tr Q9ANY1 Q9ANY1_STRPN	VPTSLAYKMA SQTIFYPFHA GDTYLRVNPQ FAVPKGTDAL VRVFDEFHGN
tr Q8DQ07 Q8DQ07_STRR6	VPTSLAYKMA SQTIFYPFHA GDTYLRVNPQ FAVPKGTDAL VRVFDEFHGN
tr Q6WNQ7 Q6WNQ7_STRPN	VPTSLAYKMA SQTIFYPFHA GDTYLRVNPQ FAVPKGTDAL VRVFDEFHGN
tr Q6WNQ5 Q6WNQ5_STRPN	VPTSLAYKMA SQTIFYPFHA GDTYLRVNPQ FAVPKGTDAL VRVFDEFHGN
tr Q9ANY1 Q9ANY1_STRPN	AYLENNYKVG EIKLPIPKLN QGTTRTAGNK IPVTTFMANAY LDNQSTYIVE
tr Q8DQ07 Q8DQ07_STRR6	AYLENNYKVG EIKLPIPKLN QGTTRTAGNK IPVTTFMANAY LDNQSTYIVE
tr Q6WNQ7 Q6WNQ7_STRPN	AYLENNYKVG EIKLPIPKLN QGTTRTAGNK IPVTTFMANAY LDNQSTYIVE
tr Q6WNQ5 Q6WNQ5_STRPN	AYLENNYKVG EIKLPIPKLN QGTTRTAGNK IPVTTFMANAY LDNQSTYIVE
tr Q9ANY1 Q9ANY1_STRPN	VPILEKENQT DKPSILPQFK RNKAQENLKL DEKVEEPKTS EKVEKEKLSE
tr Q8DQ07 Q8DQ07_STRR6	VPILEKENQT DKPSILPQFK RNKAQENSKL DEKVEEPKTS EKVEKEKLSE
tr Q6WNQ7 Q6WNQ7_STRPN	VPILEKENQT DKPSILPQFK RNKAQENSKL DEKVEEPKTS EKVEKEKLSE
tr Q6WNQ5 Q6WNQ5_STRPN	VPILEKENQT DKPSILPQFK RNKAQENSKF DEKVEEPKTS EKVEKEKLSE
tr Q9ANY1 Q9ANY1_STRPN	TGNSTSNSTL EEVPTVDPVQ EKVAKFAESY GMKLENVLFN MDGTIELYLP
tr Q8DQ07 Q8DQ07_STRR6	TGNSTSNSTL EEVPTVDPVQ EKVAKFAESY GMKLENVLFN MDGTIELYLP
tr Q6WNQ7 Q6WNQ7_STRPN	TGNSTSNSTL EEVPTVDPVQ EKVAKFAESY GMKLENVLFN MDGTIELYLP

tr Q6WNQ5 Q6WNQ5_STRPN	TGNSTSNSTL	EEVPTVDPVQ	EKVAKFAESY	GMKLENVLFN	MDGTIELYLP
tr Q9ANY1 Q9ANY1_STRPN	SGEVIKKNMA	DFTGEAPQGN	GENKPSENGK	VSTGTVENQP	TENKPADSLP
tr Q8DQ07 Q8DQ07_STRR6	SGEVIKKNMA	DFTGEAPQGN	GENKPSENGK	VSTGTVENQP	TENKPADSLP
tr Q6WNQ7 Q6WNQ7_STRPN	SGEVIKKNMA	DFTGEAPQGN	GENKPSENGK	VSTGTVENQP	TENKPADSLP
tr Q6WNQ5 Q6WNQ5_STRPN	SGEVIKKNMA	DFTGEAPQGN	GENKPSENGK	VSTGTVENQP	TENKPADSLP
tr Q9ANY1 Q9ANY1_STRPN	EAPNEKPVKP	ENSTDNGMLN	PEGNVGSDPM	LDPALEEAPA	VDPVQEKLEK
tr Q8DQ07 Q8DQ07_STRR6	EAPNEKPVKP	ENSTDNGMLN	PEGNVGSDPM	LDPALEEAPA	VDPVQEKLEK
tr Q6WNQ7 Q6WNQ7_STRPN	EAPNEKPVKP	ENSTDNGMLN	PEGNVGSDPM	LDPALEEAPA	VDPVQEKLEK
tr Q6WNQ5 Q6WNQ5_STRPN	EAPNEKPVKP	ENSTDNGMLN	PEGNVGSDPM	LDPALEEAPA	VDPVQEKLEK
tr Q9ANY1 Q9ANY1_STRPN	FTASYGLGLD	SVIFNMDGTI	ELRLPSGEVI	KKNLSDLIA	
tr Q8DQ07 Q8DQ07_STRR6	FTASYGLGLD	SVIFNMDGTI	ELRLPSGEVI	KKNLSDLIA	
tr Q6WNQ7 Q6WNQ7_STRPN	FTASYGLGLD	SVIFNMDGTI	ELRLPSGEVI	KKNLSDLIA	
tr Q6WNQ5 Q6WNQ5_STRPN	FTASYGLGLD	SVIFNMDGTI	ELRLPSGEVI	KKNLSDLIA	